

FIG. 1A

BHR (PC20  $\leq$  16 mg/ml) & Asthma

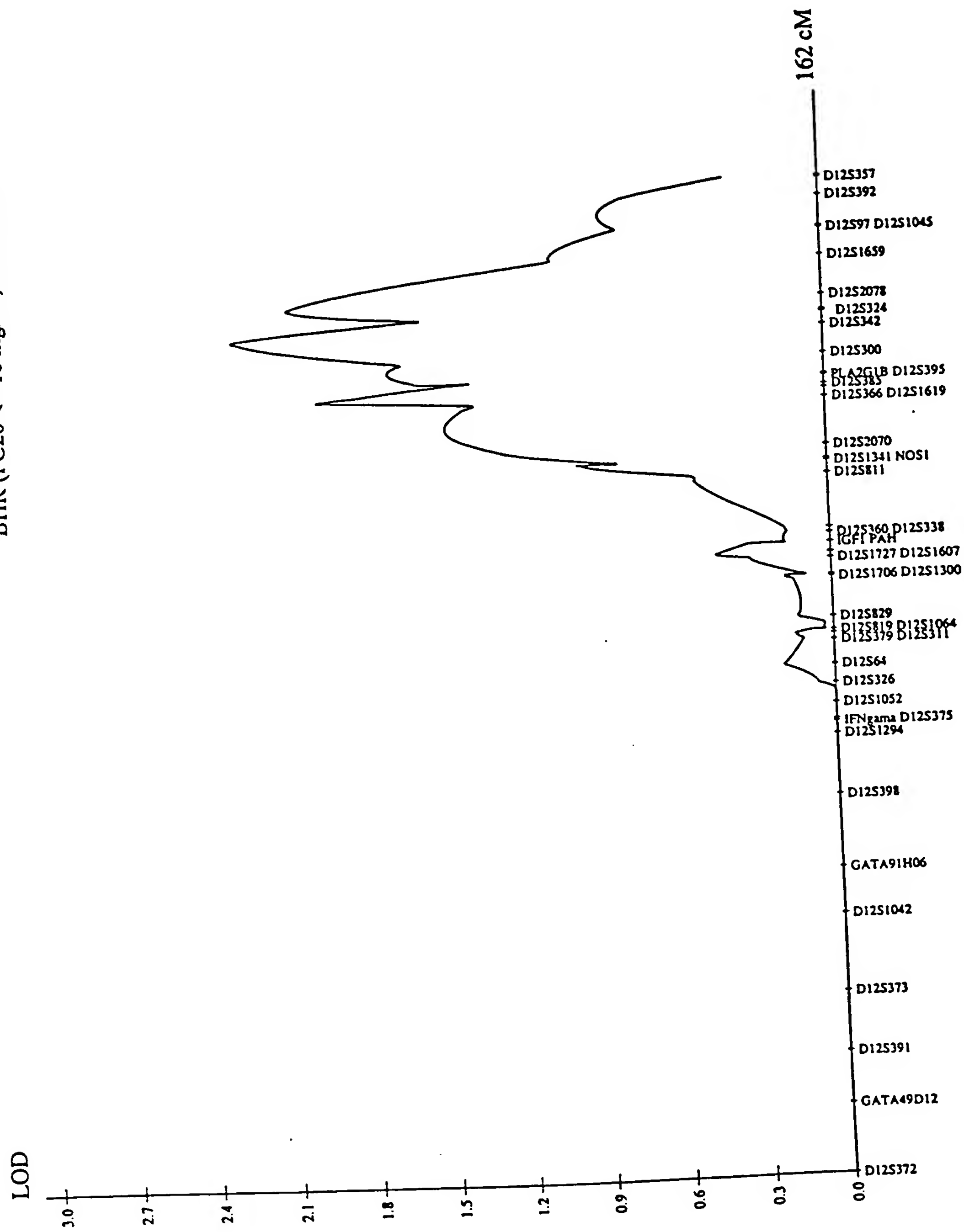


FIG. 1B

# High Total IgE & Asthma

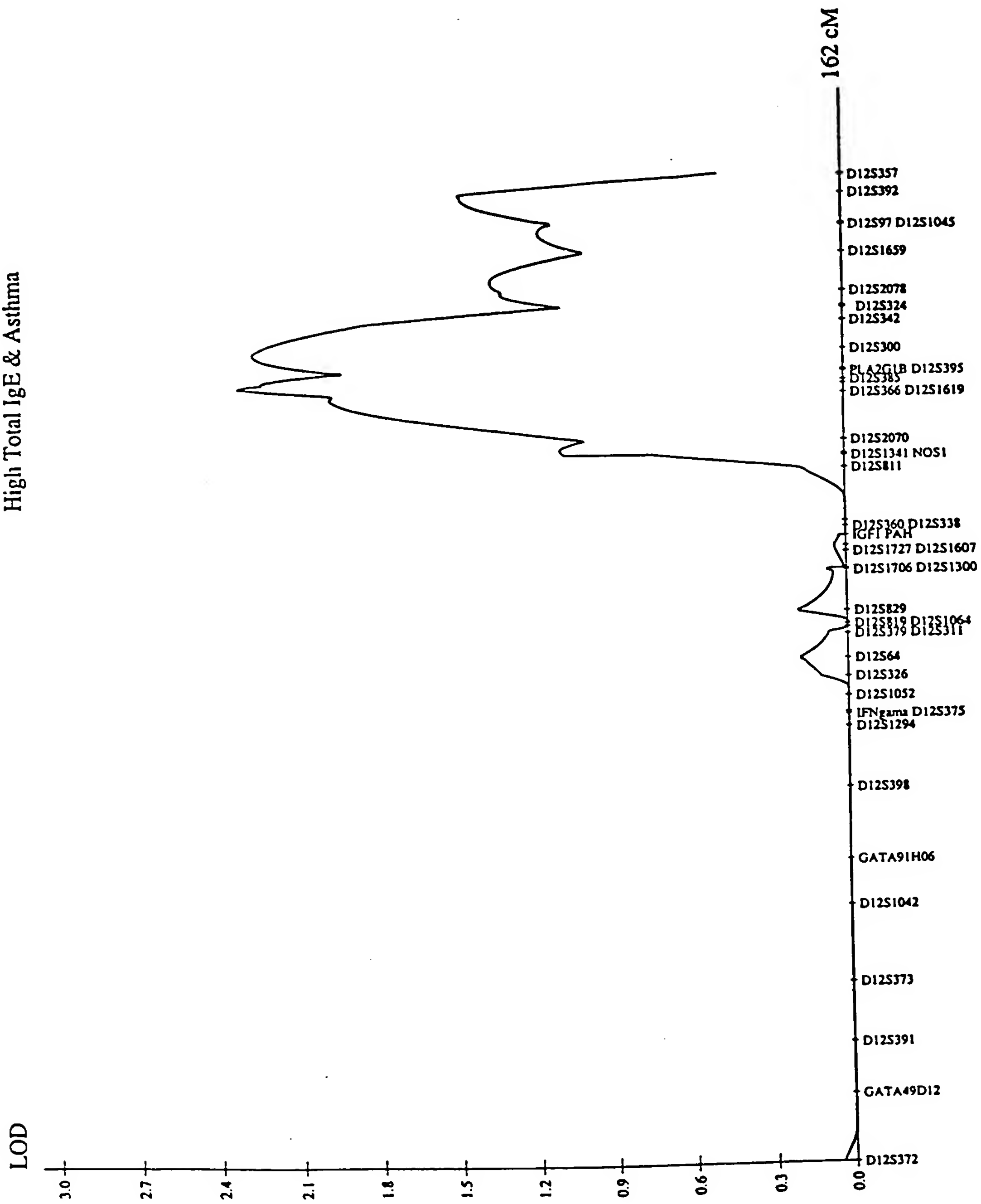


FIG. 1C

# High Specific IgE & Asthma

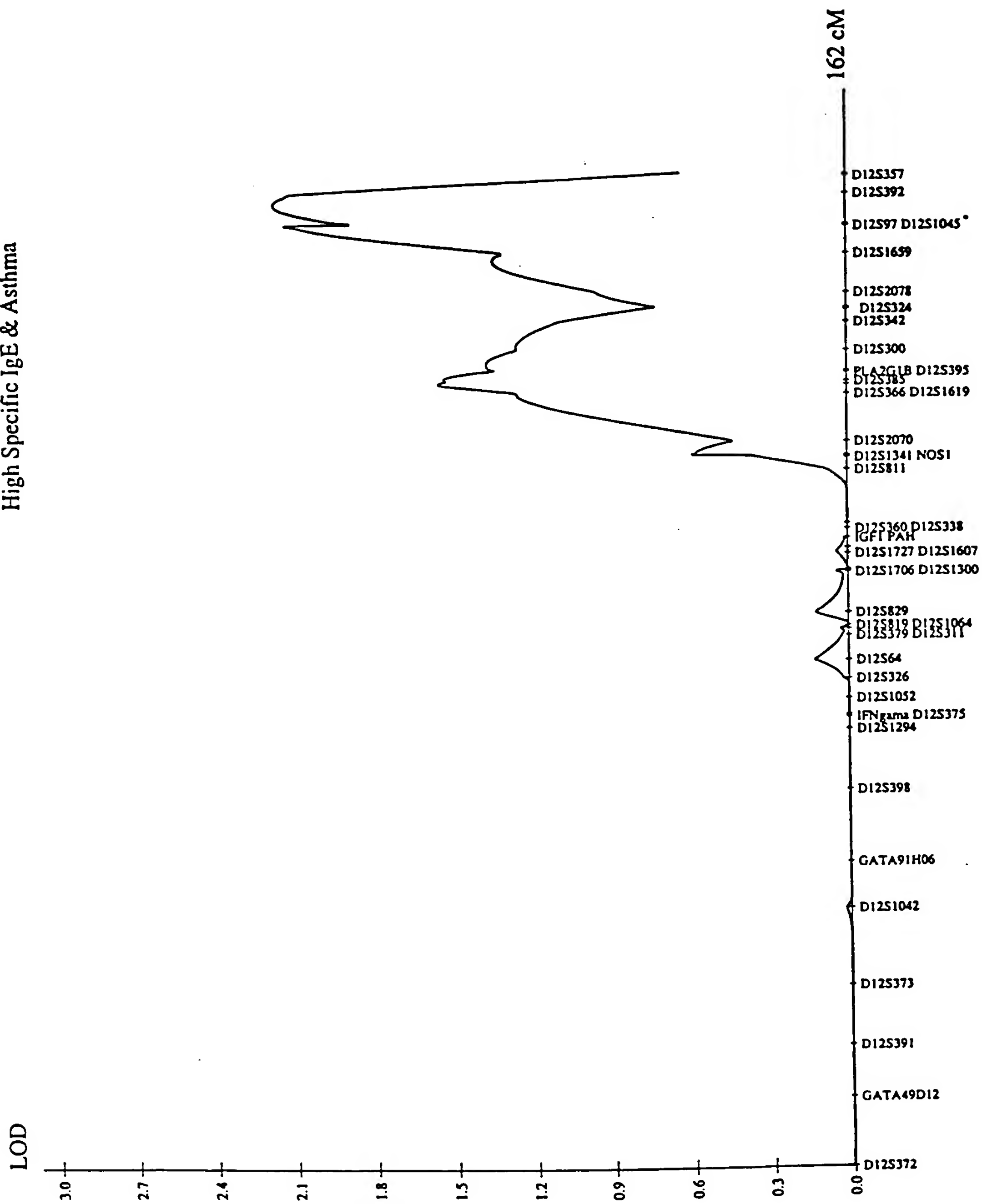
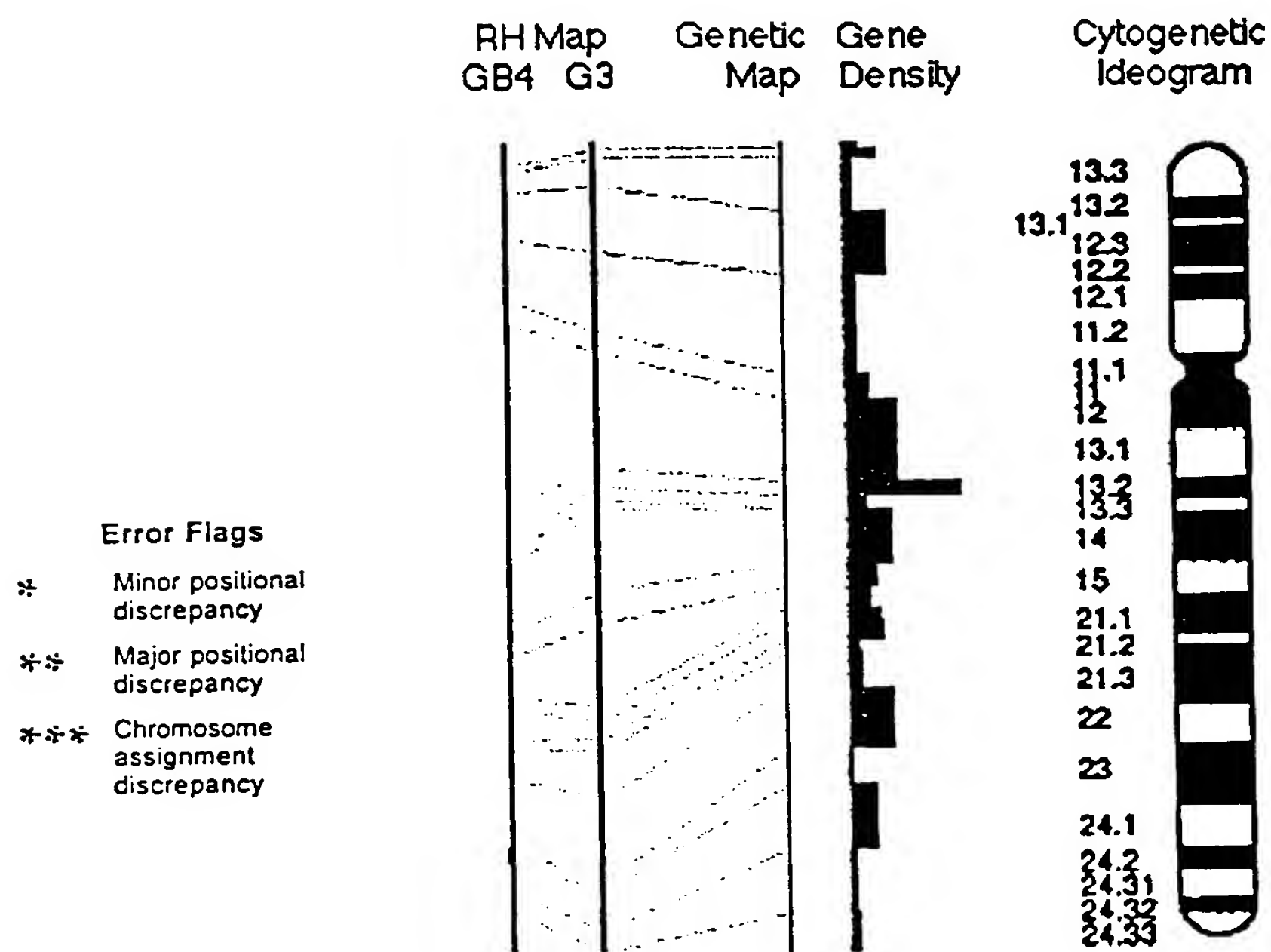


FIG. 1D



## Chromosome 12: D12S79-D12S366



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

### About This Interval

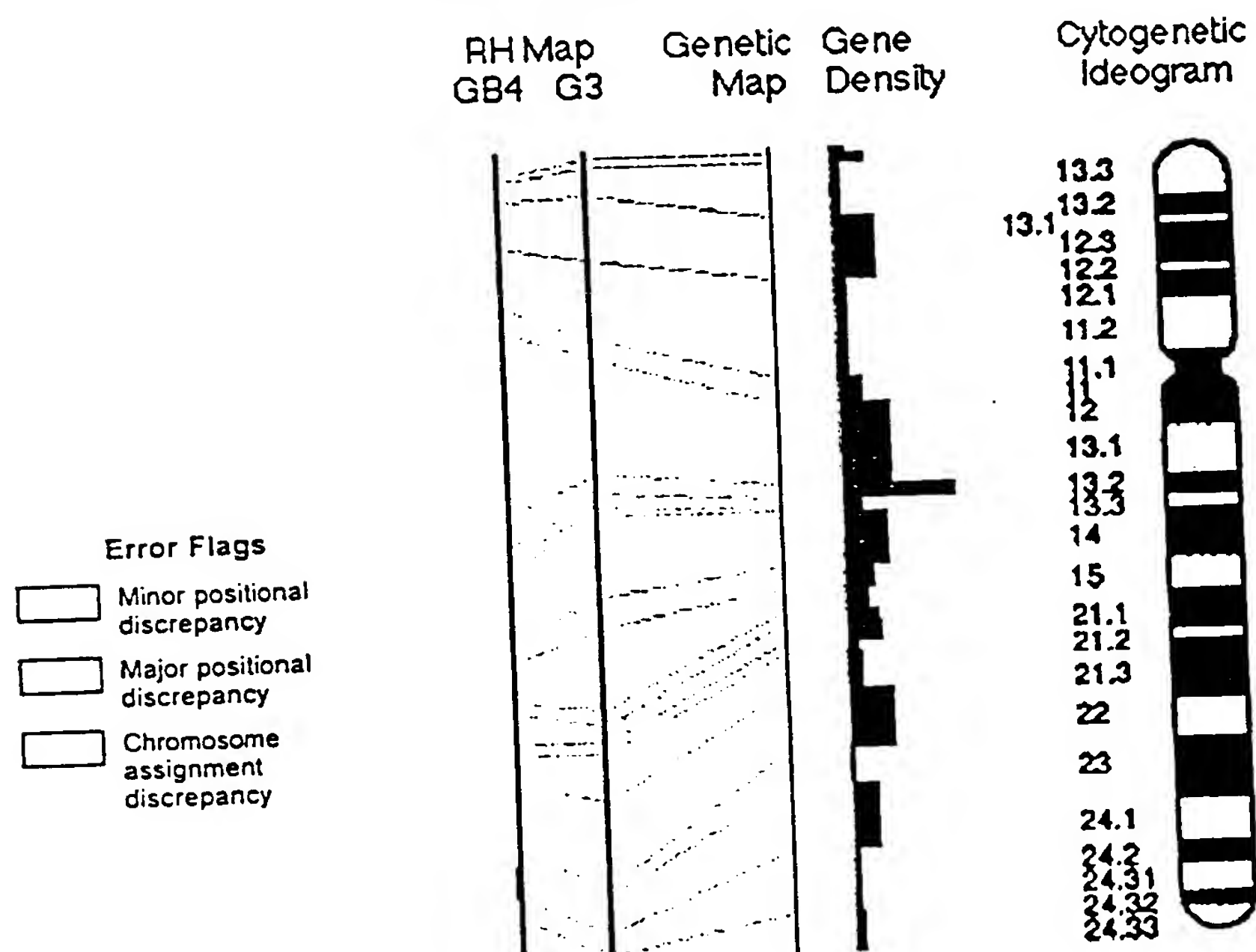
Top of interval: D12S79 (126.1 cM)  
 Bottom of interval: D12S366 (133.8 cM)  
 Genetic size of bin: 8 cM  
 Physical size of bin: 9 cR3000

**FIG. 2 A**

↑ Next interval up				
126.1	◆ 451.62 F	AFM067yc5	D12S79	Microsatellite anchor marker AFM067yc5
	454.24 P0.10	A009F32	KIAA0331	KIAA0331 gene product
	455.39 P0.37	sts-N33343		ESTs
	455.39 P1.15	SGC38179		ESTs
	455.70 P0.06	stSG54526		ESTs
	455.81 P1.35	stSG1522		ESTs
	455.86 P2.06	sts-T56610		Homo sapiens mRNA for KIAA0875 protein, p..
	456.02 P2.38	sts-R33659		EST
	456.34 P0.23	sts-D29101		EST
	456.34 P0.04 *	SGC44506		ESTs
	456.86 P2.34	NIB1804		ESTs
	456.86 P>3.00	stSG44263		ESTs, Weakly similar to calcium-binding pr..
	456.86 "	stSG62560		Homo sapiens clone 24852 mRNA sequence
	456.96 P1.66 *	sts-AA001615		ESTs
	456.96 P0.04	sts-T94297		ESTs, Weakly similar to TBX2 gene [H.sapi..
	457.17 P1.31	stSG54365		ESTs
	457.17 P0.13	WI-21497		Homo sapiens mRNA for KIAA0875 protein, p..
	457.17 P0.30	WI-20357		Homo sapiens mRNA for KIAA0875 protein, p..
	457.17 P0.38	SGC31491	NOS1	nitric oxide synthase 1 (neuronal)
	457.17 P0.31	RK903_904	NOS1	nitric oxide synthase 1 (neuronal)
	457.17 P0.18	sts-AA007571		ESTs
	457.17 P1.35	stSG46223		ESTs
	457.17 "	stSG58387		ESTs
	◆ 457.27 P>3.00 *	Cdalce05		Homo sapiens clone 23714 mRNA sequence
	457.27 P0.10 *	sts-W79390	NME2	non-metastatic cells 2, protein (NM23B) exp..
	457.48 P0.20	sts-Z40829		ESTs
	460.94 P0.00 *	A005Q47		ESTs
133.8	◆ 460.94 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
↓ Next interval down				

FIG. 2 B

## Chromosome 12: D12S366-D12S340



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

### About This Interval

Top of interval: D12S366 (133.8 cM)

Bottom of interval: D12S340 (147.5 cM)

Genetic size of bin: 14 cM

Physical size of bin: 21 cR3000

↑ Next interval up				
133.8	◆ 460.94 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
	462.85 P1.00 *	stSG8109		ESTs
	462.85 "	sts-X75252	PBP	prostatic binding protein
	462.95 P1.04	sts-AA011374		Homo sapiens KIAA0431 mRNA, partial cds

FIG. 2 C

463.77 P0.19	WI-16745		Human clone 37, 5cM region surrounding hepa..
◆ 463.77 P0.20	SGC33949	KIAA0262	KIAA0262 gene product
463.98 P0.02	A008B04		ESTs
463.98 "	stSG50309		ESTs
463.98 "	stSG49970		Homo sapiens mRNA for KIAA0875 protein, p..
463.98 P0.04	stSG27318		Human clone 23932 mRNA sequence
463.98 P0.08	R06295		EST
463.98 P1.33	sts-W56792		ESTs
464.08 P2.32	A007E48		ESTs
464.19 P1.28	A009U43		ESTs
464.29 P1.33	stSG3138		Homo sapiens mRNA for KIAA0949 protein, p..
464.39 P1.09	sts-F21636		Human DNA sequence from BAC 15E1 on chrom..
464.39 P1.13	stSG15685	KIAA0262	KIAA0262 gene product
464.39 "	RP_P0_1	RPLP0	Ribosomal protein large, P0
464.39 P1.09	stSG29626		ESTs
464.39 P1.14	stSG31407		Human DNA sequence from BAC 15E1 on chrom..
464.39 "	A001T32	PXN	paxillin
464.39 "	A001W18		H.sapiens mRNA for AMP-activated protein ..
464.39 "	WIAF-40		Human mRNA for KIAA0219 gene, partial cds
464.39 "	sts-T95105		ESTs
464.39 "	Cda0id01		ESTs
464.39 P1.13	stSG31431		ESTs, Moderately similar to (defline not a..
◆ 464.39 " *	WI-13177		Homo sapiens clone 23714 mRNA sequence
464.39 "	IB1092		Homo sapiens clone 23714 mRNA sequence
464.39 "	T79466		ESTs
464.39 P1.18	stSG48379		ESTs
464.45 P1.05	KIAA0219		Human mRNA for KIAA0219 gene, partial cds
464.45 "	stSG40392		ESTs
464.45 "	stSG31586		H.sapiens mRNA for AMP-activated protein ..
◆ 464.49 P0.21	A006F12	KIAA0152	KIAA0152 gene product
464.49 P0.25	sts-AA002185	PXN	paxillin
464.49 P0.10	stSG48442		ESTs
464.49 "	sts-T16456		ESTs
464.49 "	stSG62260		ESTs

FIG. 2 D

	464.49 "	NIB1331		ESTs
	464.49 "	WI-15518		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49 "	WIAF-1058		ESTs, Moderately similar to unknown [H.sapi..
	464.49 "	SGC34758		ESTs
	464.49 "	WI-19738		Homo sapiens mRNA for KIAA0787 protein, p..
	464.49 "	IB383		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49 "	SGC32343		ESTs
	464.79 P0.96	SGC33521		ESTs
	464.79 P0.96 *	X58965	NME2	non-metastatic cells 2, protein (NM23B) exp..
	465.20 P0.20	sts-H10302		ESTs
◆	465.38 P0.85	A007E11	KIAA0262	KIAA0262 gene product
	465.41 P0.81	A007I44	RPLP0	ribosomal protein, large, P0
	465.41 "	stSG22726		EST
	465.41 "	WI-17776		ESTs
	465.41 "	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41 "	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41 P0.77	stSG4775	SFRS9	splicing factor, arginine/serine-rich 9
	465.41 "	A002J47		ESTs, Weakly similar to heat shock protein..
	465.41 P0.80	stSG46660		EST
	465.51 P0.75	stSG41086	PXN	paxillin
	465.51 P0.83	stSG52121		ESTs
	465.91 P0.01	WI-16071		ESTs
	465.91 P0.00	WI-13962		H.sapiens mRNA for AMP-activated protein ..
	466.62 P0.00	sts-AA011220	SFRS9	splicing factor, arginine/serine-rich 9
	466.71 P0.00	stSG4712		ESTs, Weakly similar to homology with o251..
	466.91 P0.01	WI-15135		Homo sapiens mRNA for KIAA0787 protein, p..
	466.91 P0.01	D12S2088	TCF1	transcription factor 1, hepatic; LF-B1, hep..
	467.01 P0.01	stSG52567		ESTs
135.1	467.11 F	AFM123xh2	D12S86	Microsatellite marker AFM123xh2
135.1	467.11 P0.01	AFM299zd5	D12S349	Microsatellite marker AFM299zd5
	467.11 P0.01	AFM123xh2		Unknown
137.5	◆ 467.21 P0.02	AFM220zf4	D12S321	Microsatellite marker AFM220zf4
	467.21 P0.02	sts-W73277	SFRS9	splicing factor, arginine/serine-rich 9
	467.21 P0.02	stSG8721		EST

FIG. 2 E

467.21 "	stSG44224		ESTs
467.21 "	stSG49978		H.sapiens mRNA for AMP-activated protein ..
◆ 467.21 "	stSG31862		Homo sapiens HSPC004 mRNA, complete cds
467.21 "	stSG47820		ESTs
467.21 "	Bdac4h06	KIAA0262	KIAA0262 gene product
467.21 "	stSG15021		ESTs
467.21 "	A002B13	SFRS9	splicing factor, arginine/serine-rich 9
◆ 467.21 "	H50549	KIAA0262	KIAA0262 gene product
467.21 P0.03	SGC35167		EST
467.21 P0.03	WI-19637		H.sapiens mRNA for AMP-activated protein ..
467.21 P0.02	WIAF-607		Unknown
467.31 P0.02	WI-16997	RPLP0	ribosomal protein, large, P0
468.93 P0.85	SGC31344		EST
469.13 P0.90	A007C39	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 ..
469.13 P0.14	stSG35104		ESTs
469.13 "	A006Q41		Unknown
469.23 P0.18	sts-Y07684	P2RX4	purinergic receptor P2X, ligand-gated ion c..
469.33 P0.93	stSG8506		ESTs, Moderately similar to unknown [H.sap..
469.33 "	R01708		EST
469.33 "	stSG54819	HCALB_BR	calbrain
469.33 "	A001Z45		ESTs, Highly similar to (define not avail..
469.33 "	stSG35318		ESTs, Weakly similar to fos39554 1 [H.sapi..
469.33 "	stSG63173		EST
469.33 "	stSG31374	OASL	2'-5'oligoadenylate synthetase-like
469.42 P1.01	WI-16068		EST
469.44 P0.23	stSG1961		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62627		EST
469.44 "	stSG36007		Homo sapiens full length insert cDNA clone..
469.44 "	stSG39281	P2RX7	purinergic receptor P2X, ligand-gated ion c..
469.44 "	stSG2554		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62591		ESTs
◆ 469.54 P1.03	A006N38	KIAA0152	KIAA0152 gene product
469.62 P1.03	sts-N34573		ESTs
469.62 P1.03	sts-N58045		ESTs

FIG. 2 F

469.62 P1.04	WI-13224		EST
469.83 P1.12	SGC34424		ESTs
469.93 P1.14	stSG3875	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.14 P1.17	stSG52516		ESTs, Weakly similar to (define not avail..
470.24 P1.32	D0S1735E		ESTs
470.24 P1.12	WI-6178		ESTs
470.32 P1.25	sts-U29895		Unknown
470.32 P1.24	WI-19611	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.43 P1.29	stSG52094		ESTs
470.63 P1.38	A004O17		ESTs
◆ 470.77 P1.32 **	SGC33451		ESTs, Weakly similar to rhoHP1 [H.sapiens..
◆ 470.84 P1.35 **	sts-X64838	RSN	restin (Reed-Steinberg cell-expressed inter..
470.84 P1.52	WI-13062		Homo sapiens mRNA, expressed in fibroblast..
471.27 P1.60	sts-R99269		EST
471.37 P1.70	stSG1991		ESTs
471.37 "	stSG15859		Homo sapiens full length insert cDNA YQ02..
471.58 P1.78	stSG29729		ESTs, Weakly similar to (define not avail..
471.58 P1.37	WI-16979		ESTs
471.65 P1.39	WI-17693		EST
471.80 P1.29	WI-22060		ESTs
471.90 P>3.00	stSG8210		ESTs, Moderately similar to neuronal threa..
471.90 "	WI-17956		EST
471.90 "	WI-20969		Homo sapiens mRNA for KIAA0867 protein, c..
471.90 "	stSG47029		ESTs
471.90 "	stSG47647		EST
471.90 "	sts-W45376		Homo sapiens mRNA for KIAA0867 protein, c..
◆ 471.90 " **	WI-6021	RSN	restin (Reed-Steinberg cell-expressed inter..
471.90 "	NIB962		ESTs
471.90 "	A009E34		ESTs, Moderately similar to neuronal threa..
471.90 "	sts-T17477		ESTs
472.08 P1.49	sts-X89984		H.sapiens mRNA for BCL7A protein
472.12 P>3.00	SGC34693		EST
472.12 P>3.00	A009O01		ESTs, Weakly similar to neuronal thread pr..
472.29 P>3.00	stSG47084		ESTs

FIG. 2 G



472.40 P>3.00	stSG58209	EEF1D	eukaryotic translation elongation factor 1 d..
472.40 P>3.00	AA213821	EEF1D	eukaryotic translation elongation factor 1 d..
472.61 P>3.00	A002R44		Unknown
472.61 P>3.00	SGC35850	EEF1D	eukaryotic translation elongation factor 1 d..
472.72 P0.01	sts-H98108		ESTs
472.97 P>3.00	WI-6239		ESTs
473.04 P>3.00	sts-H75490		ESTs
◆ 473.58 P>3.00 **	WI-14983	RSN	restin (Reed-Steinberg cell-expressed inter..
474.01 P>3.00	stSG8610		ESTs
474.01 P>3.00	stSG47080		ESTs
474.38 P2.18	stSG8686		ESTs, Weakly similar to similar to pre-mRN..
474.38 P2.25	stSG26358		ESTs, Weakly similar to similar to pre-mRN..
474.38 "	stSG29931		ESTs
474.38 "	WI-17926		ESTs
474.38 "	WI-12790		ESTs, Weakly similar to MULTIDRUG RESI..
474.38 "	1834		EST
474.38 P2.26	sts-X98258	MPP-9	M phase phosphoprotein 9
474.38 P2.39	stSG40753		ESTs
474.64 P>3.00	A004D47		ESTs, Highly similar to There are three pu..
474.64 P>3.00	sts-N23129	MPP-9	M phase phosphoprotein 9
474.75 P2.41	sts-AA040696		ESTs
474.81 P2.37	sts-AA022496		ESTs
474.81 P2.28	stSG46930	MPP-9	M phase phosphoprotein 9
474.97 P>3.00	WI-20552	DRP	density-regulated protein
475.02 P>3.00	SGC30324		ESTs
475.07 P>3.00	D10923	HM74	putative chemokine receptor; GTP-binding pr..
475.07 P>3.00	stSG2418	DOC1	Deleted in oral cancer-1
475.07 "	stSG21321		ESTs
475.07 "	stSG53515	MPP-9	M phase phosphoprotein 9
475.07 P>3.00	SGC31687	DOC1	Deleted in oral cancer-1
475.07 P>3.00	WIAF-214	HM74	putative chemokine receptor; GTP-binding pr..
475.13 P0.79	sts-W93806		ESTs
475.13 P2.13	stSG48145		ESTs
475.18 P2.34	A003B12		Homo sapiens full length insert cDNA clone..

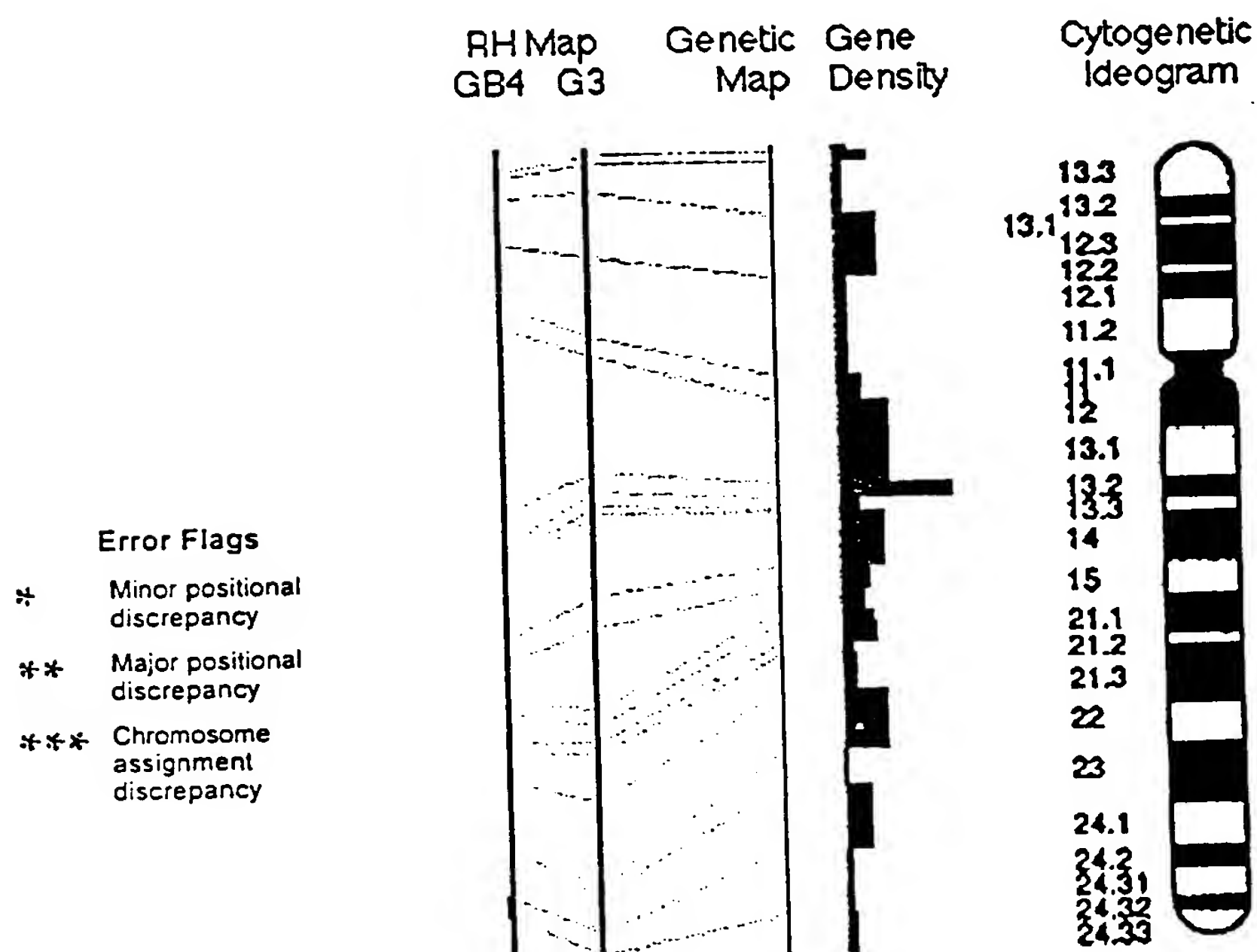
FIG. 2 H



	475.18 P>3.00	WI-22211		Homo sapiens full length insert cDNA clone..
	475.18 P2.08	stSG48093		ESTs
	475.18 "	A004P27		ESTs, Weakly similar to MULTIDRUG RESI..
	475.35 P2.10	stSG9904		ESTs
	475.40 P0.45	sts-AA024696		ESTs
	475.51 P>3.00	stSG53793		ESTs
	476.10 P>3.00	Bda98d05		Homo sapiens full length insert cDNA clone..
	476.21 P>3.00	sts-H24468		ESTs
	476.21 P>3.00	sts-N94741		ESTs
	476.64 P0.28	stSG22488		ESTs
	476.85 P0.36	stSG44909		ESTs
	477.06 P0.10	stSG54797		ESTs
	477.27 P1.33	stSG48099		ESTs
	477.37 P0.09 *	sts-AA028894		Homo sapiens silencing mediator of retinoic..
	477.80 P1.44	stSG52727		EST
	477.80 "	U44799		Human U1-snRNP binding protein homolog mR..
	477.80 "	WI-15963		ESTs
	477.80 "	stSG53886		ESTs, Weakly similar to neuronal thread pr..
	478.74 P0.01	WIAF-364		ESTs
	479.01 P0.21	WI-21080		ESTs
	479.13 P0.19	A009B29		ESTs
	479.33 P0.22	A006F32	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33 P0.19	WIAF-449	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33 P0.19 *	WI-15890		H.sapiens mRNA for transmembrane protein r..
	479.55 P0.20 *	stSG349		H.sapiens mRNA for transmembrane protein r..
	479.55 " *	A004O46	BDKRB2	bradykinin receptor B2
	479.55 "	stSG42540		ESTs
	479.55 "	sts-N26791		ESTs
	479.55 "	stSG53943		ESTs
	479.55 "	stSG49468		EST
145.7	479.74 P0.16	AFM294ze9	D12S342	Microsatellite marker AFM294ze9
	481.46 P0.00	sts-AA007694		EST
147.5	481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1
	Next interval down			

FIG. 2 I

## Chromosome 12: D12S340-D12S97



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

### About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

Physical size of bin: 13 cR3000

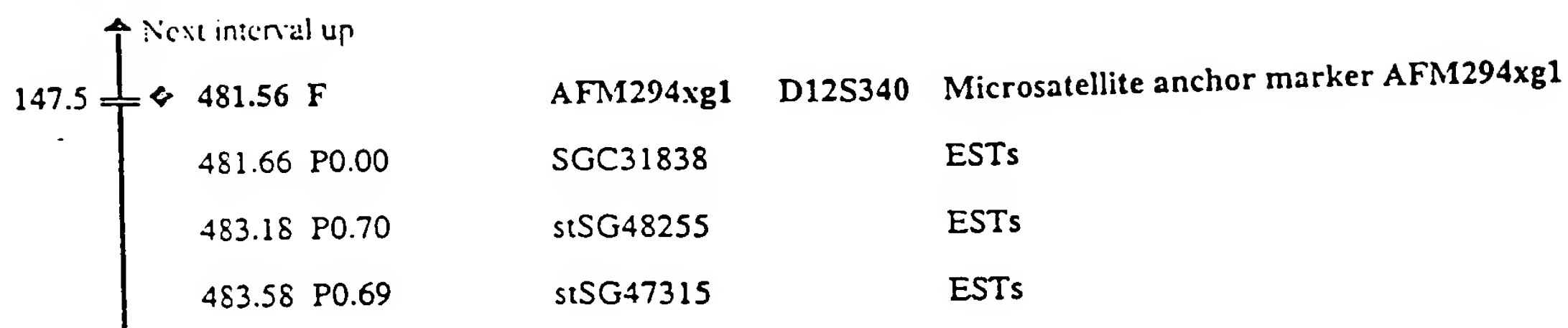


FIG. 2 J

483.87 P0.83	stSG47707	ESTs
484.70 P0.93	stSG4060	ESTs
484.70 "	stSG62390	GTF2H3 general transcription factor IIIH, polypepti..
484.70 "	stSG42994	ESTs
484.73 P0.74	stSG46906	ESTs
484.80 P0.91	A004X33	ESTs
484.91 P1.11	stSG3211	ESTs, Weakly similar to B-cell growth fact..
484.91 " *	sts-Z41302	BDKRB2 bradykinin receptor B2
484.91 " *	sts-Z41302	BDKRB2 bradykinin receptor B2
484.91 "	sts-T58259	ESTs, Weakly similar to B-cell growth fact..
484.91 "	stSG52737	ESTs
484.91 "	Bda03b10	UBC ubiquitin C
484.91 "	stSG1936	CD36L1 CD36 antigen (collagen type I receptor, thr..
484.91 "	sts-AA017225	ESTs
484.91 P1.15	WI-12212	ESTs
485.12 P1.18	A004F14	ESTs
485.12 P1.18	SGC31333	ESTs
485.23 P1.21 *	WI-12482	BDKRB2 bradykinin receptor B2
485.23 P1.07	sts-AA017698	ESTs
485.33 P1.22	WI-12422	ESTs
485.51 P1.18	stSG42398	EST
485.64 P1.04	sts-AA009669	ESTs
486.07 P2.50	stSG21539	EST
486.13 P1.44	WI-12439	EST
486.34 P1.26	sts-W31616	UBC ubiquitin C
486.38 P>3.00	stSG54715	ESTs
486.76 P1.64 *	WI-6921	H.sapiens mRNA for transmembrane protein r..
487.08 P>3.00	WI-13120	Human mRNA for KIAA0318 gene, partial cds
487.23 P>3.00	stSG54353	ESTs
487.23 P>3.00	stSG22703	EST
487.28 P>3.00	stSG62698	ESTs
487.28 P>3.00 *	sts-D60472	Homo sapiens silencing mediator of retinoic..
487.28 P>3.00	stSG36097	ESTs
487.33 P1.36	sts-U37146	Homo sapiens silencing mediator of retinoic..

FIG. 2 K

	487.50 P>3.00	stSG9807	ESTs
	487.50 P>3.00	stSG15434	ESTs
	487.60 P>3.00	stSG53251	ESTs
	487.60 P>3.00	stSG30525	SRRP129 SC35-interacting protein 1
	487.60 P>3.00	stSG46424	ESTs
	487.70 P>3.00	A007A34	ESTs
154.4	487.75 P2.00	AFMa197zd9	D12S1609 Microsatellite marker AFMa197zd9
	487.75 P2.02	A006D44	ESTs
	487.80 P>3.00	SGC30248	ESTs, Weakly similar to peptide/histidine ..
	488.07 P1.68	stSG6320	Homo sapiens clone 24617 mRNA sequence
	488.07 P1.66	stSG6305	Homo sapiens clone 24790 mRNA sequence
	488.07 P0.02	sts-N20163	Homo sapiens full length insert cDNA clone..
	488.12 P>3.00	stSG60065	ESTs
	488.12 P>3.00	stSG47723	ESTs
	488.44 P1.59	stSG3292	Homo sapiens clone 24790 mRNA sequence
	488.44 P0.03	WIAF-856	EST, Weakly similar to reverse transcripta..
	488.65 P1.54	WI-12272	Homo sapiens clone 24790 mRNA sequence
	488.65 P1.82	stSG52343	ESTs
	488.82 P1.80	stSG16387	CPN2 carboxypeptidase N, polypeptide 2, 83kD
	488.97 P1.80	SGC31722	ESTs
	489.07 P0.06	stSG54325	ESTs
	489.07 P>3.00	stSG63473	ESTs
160.9	◆ 489.07 P>3.00	AFMa123xe1	D12S367 Microsatellite marker AFMa123xe1
	489.14 P0.17	sts-T81113	ESTs
	489.29 P0.05	sts-AA025438	EST
	489.50 P1.37	*** Cdalad08	ESTs
	489.50 P0.05	WI-15018	ESTs
	489.50 P1.50	WI-18492	ESTs
	489.57 P1.48	WI-16177	Homo sapiens androgen receptor associated p..
	489.67 P1.44	stSG53307	ESTs
	489.71 P1.43	stSG53541	Homo sapiens hiwi mRNA, partial cds
	489.71 P1.43	stSG9546	Homo sapiens clone 24617 mRNA sequence
	489.89 P1.56	A006O16	ESTs
	490.10 P1.42	H64839	EST

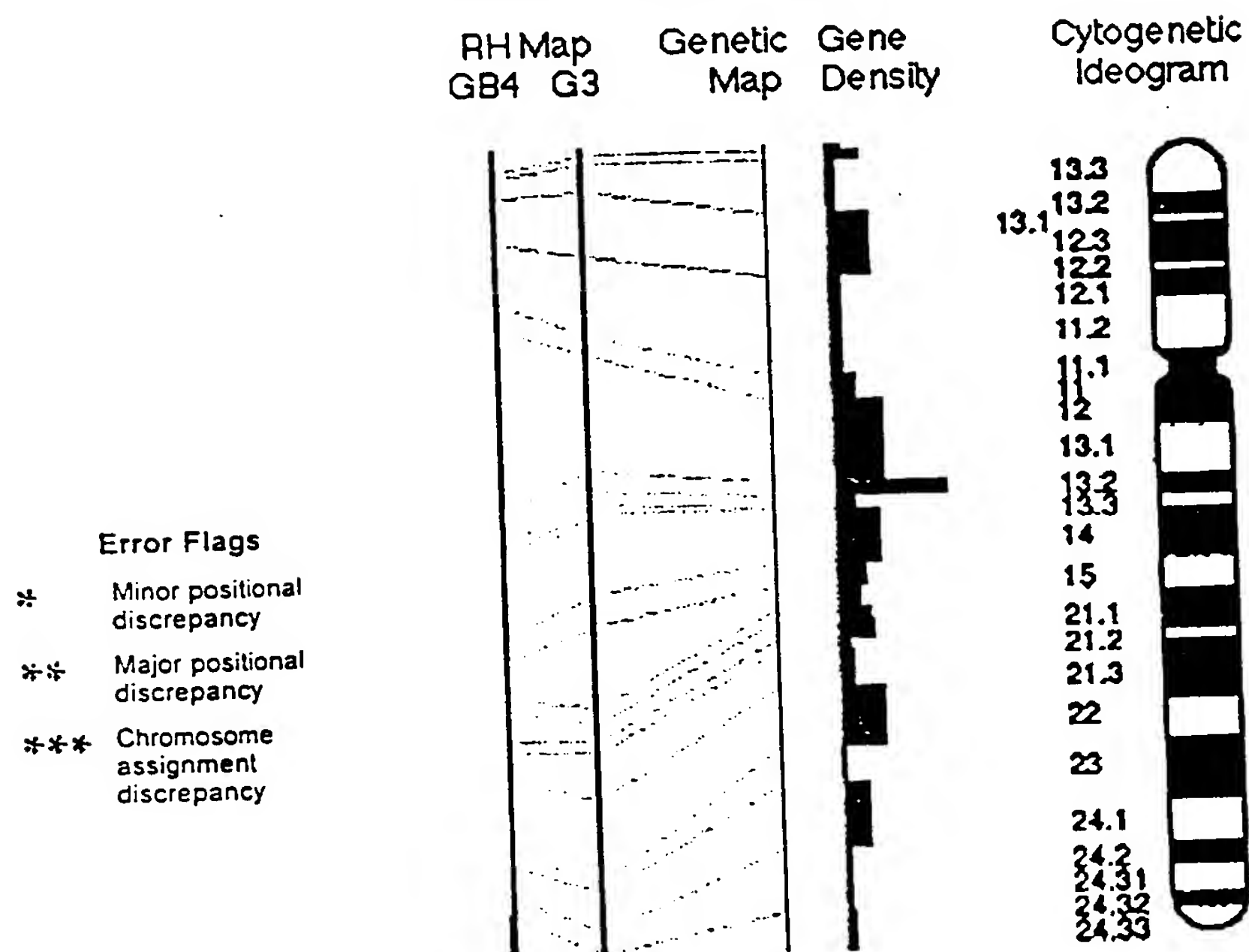
FIG. 2 L

160.9 — 490.20 P0.05  
— ♦ 494.19 F  
↓ Next interval down

stSG43910	SFRS8	splicing factor, arginine/serine-rich 8 (sup..
AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6

FIG. 2 M

## Chromosome 12: D12S97-qTEL



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

### About This Interval

Top of interval: D12S97 (160.9 cM)  
 Bottom of interval: chr12\_qTEL (169.1 cM)  
 Genetic size of bin: 8 cM  
 Physical size of bin: 172 cR3000

Next interval up				
160.9	◆ 494.19 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6
	498.06 P0.02	stSG53600		ESTs, Weakly similar to peptide/histidine ..
	499.71 P1.73	stSG3357		ESTs
165.7	499.71 "	AFM295ye9	D12S343	Microsatellite marker AFM295ye9

FIG. 2 N

499.71 P1.72	stSG30906	ESTs	
499.71 "	stSG43796	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.71 P1.71	sts-X89576	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.92 P>3.00	stSG43769	ESTs	
500.50 P1.88	stSG26056	ESTs	
500.50 P2.33	SGC30786	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG1702		Homo sapiens CAGH32 mRNA, partial cds
500.61 "	sts-N59820	ESTs	
500.61 "	stSG42115	KIAA0331	KIAA0331 gene product
500.61 "	IB2452	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 "	stSG52521	ESTs	
500.61 "	FB9F8		ESTs, Weakly similar to PUTATIVE ATP-D..
500.61 "	AA252357	ESTs	
500.61 "	stSG4720		Homo sapiens pseudouridine synthase 1 (PUS..
500.61 "	sts-AA001424	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG31443	ESTs	
500.61 P>3.00	stSG49622	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 P2.49	stSG50559	ESTs	
501.04 P1.10	stSG54842	ESTs	
501.04 P2.03	A008Y05	Unknown	
501.89 P2.18	stSG39493		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	A002A44		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	sts-H94865	EST	
501.99 P>3.00	R50113	ESTs	
502.10 P1.75	stSG48386	ESTs	
502.10 "	stSG50504	ESTs	
502.63 P0.06	A006R19	ESTs	
502.63 P1.06	WIAF-864	ESTs	
502.94 P1.51	stSG54813		ESTs, Weakly similar to peroxisome membran..
503.04 P1.42	A004B47		ESTs, Highly similar to DNA polymerase ep..
503.25 P0.28	stSG27206	ESTs	
503.25 "	stSG40199		Homo sapiens mRNA for KIAA0692 protein, p..
503.46 P0.23	stSG8935	ESTs	
504.68 P0.69	stSG4731		Homo sapiens mRNA for KIAA0692 protein, p..

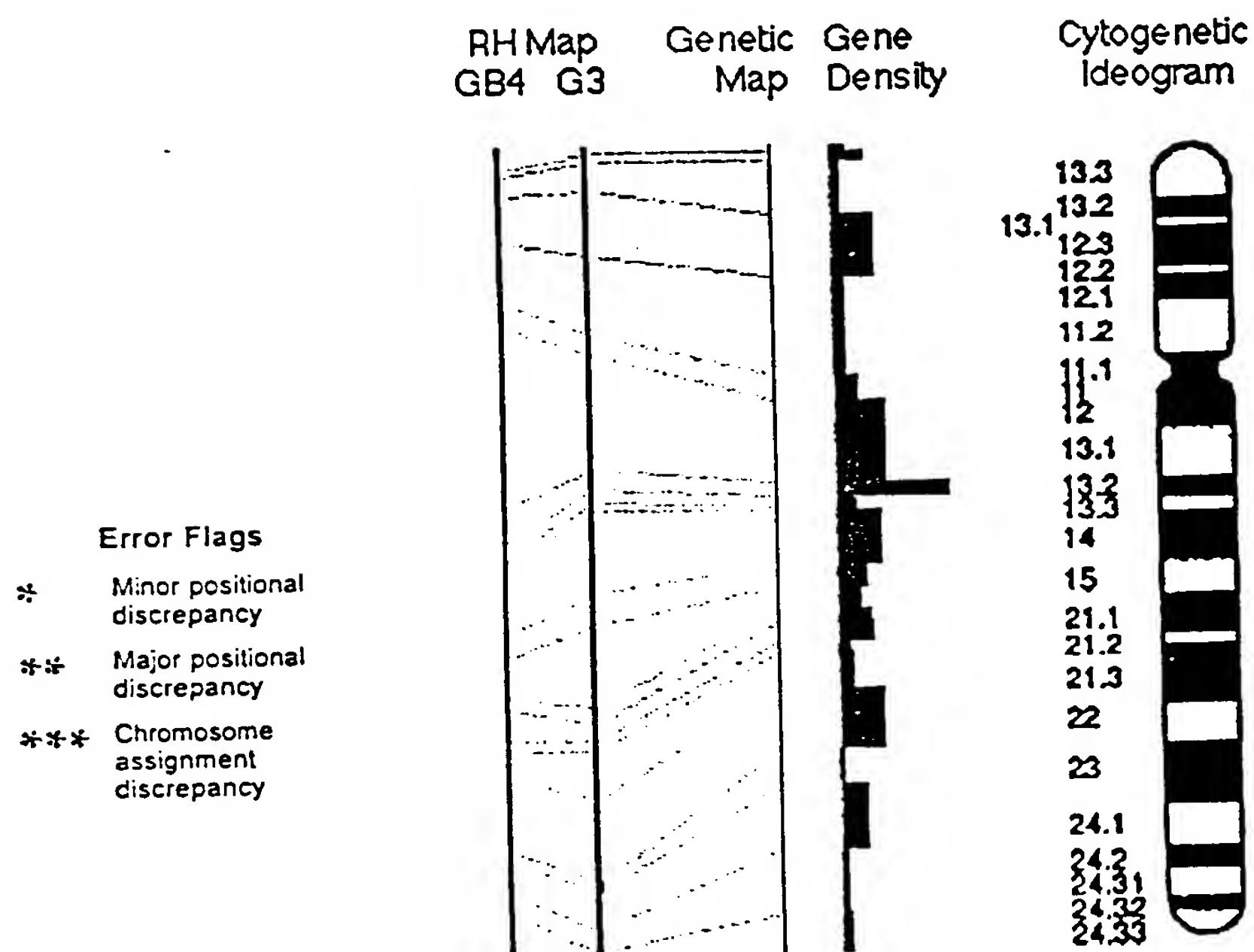
FIG. 2 O

169.1	504.68 "	A005Q05		ESTs
	504.68 "	stSG8142		ESTs, Highly similar to DNA polymerase ep..
	506.39 F	AFM310vd5	D12S357	Microsatellite marker AFM310vd5
	506.39 P0.02	A005X42		Homo sapiens mRNA for KIAA0692 protein, p..
	508.59 P0.78	Cda18g06		ESTs
	◆ 508.59 P0.78 **	Cda1jf08		Homo sapiens mRNA for GCP170, complete cd..
	508.59 P0.54	R39599		ESTs
	509.98 P0.10	stSG31494	ZNF140	zinc finger protein 140 (clone pHZ-39)
	509.98 P0.16	stSG40222		ESTs
	509.98 "	sts-R55615		ESTs, Weakly similar to zinc finger protei..
	509.98 "	sts-R02295		ESTs
	509.98 "	sts-R81342		ESTs
	511.20 F	TEL-12q82		Marker TEL-12q82
	512.81 P0.20	sts-H65839		ESTs, Weakly similar to transformation-rel..
	514.97 P0.36	stSG46141		ESTs, Weakly similar to zinc finger protei..
	514.97 P0.90	stSG52998		ESTs
	519.10 P1.77	A008W21	CYP51	cytochrome P450, 51 (lanosterol 14-alpha-de..
	519.54 P0.81	stSG52716		ESTs
● TELOMERE				

FIG. 2 P



## Chromosome 12: D12S79-D12S366



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

### About This Interval

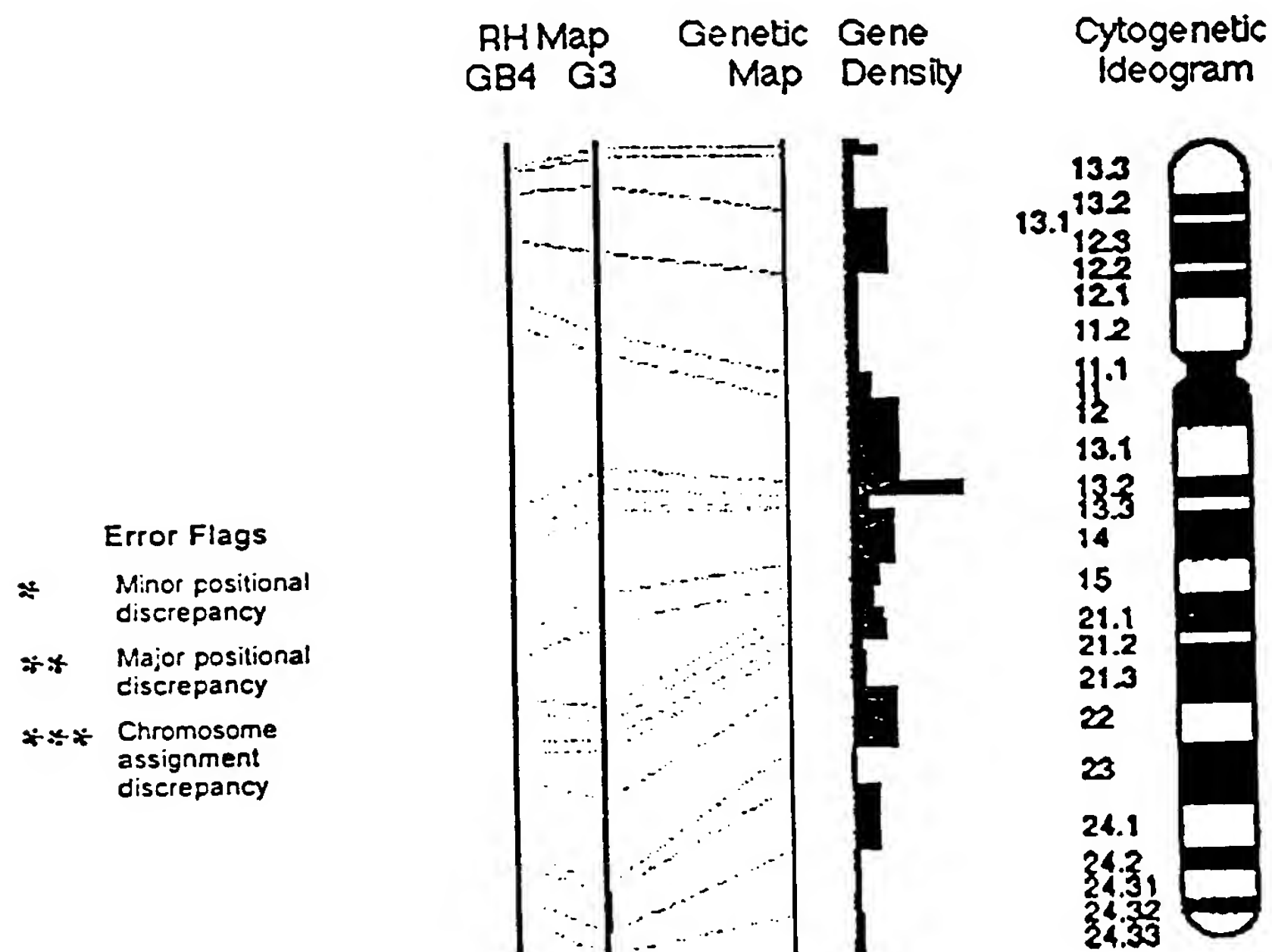
Top of interval: D12S79 (126.1 cM)  
 Bottom of interval: D12S366 (133.8 cM)  
 Genetic size of bin: 8 cM  
 Physical size of bin: 63 cR10000

FIG. 3 A

↑ Next interval up				
126.1	◆ 4955 F	AFM067yc5	D12S79	Microsatellite anchor marker AFM067yc5 (SHGC-692)
129.2	4988 F	AFMa067we1	D12S1718	Microsatellite marker AFMa067we1 (SHGC-20..
	◆ 5007 F *	SHGC-2657		Homo sapiens clone 23714 mRNA sequence
	◆ 5014 F *	SHGC-2653		Homo sapiens clone 23714 mRNA sequence
133.8	◆ 5018 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)
↓ Next interval down				

FIG. 3 B

## Chromosome 12: D12S366-D12S340



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

### About This Interval

Top of interval: D12S366 (133.8 cM)

Bottom of interval: D12S340 (147.5 cM)

Genetic size of bin: 14 cM

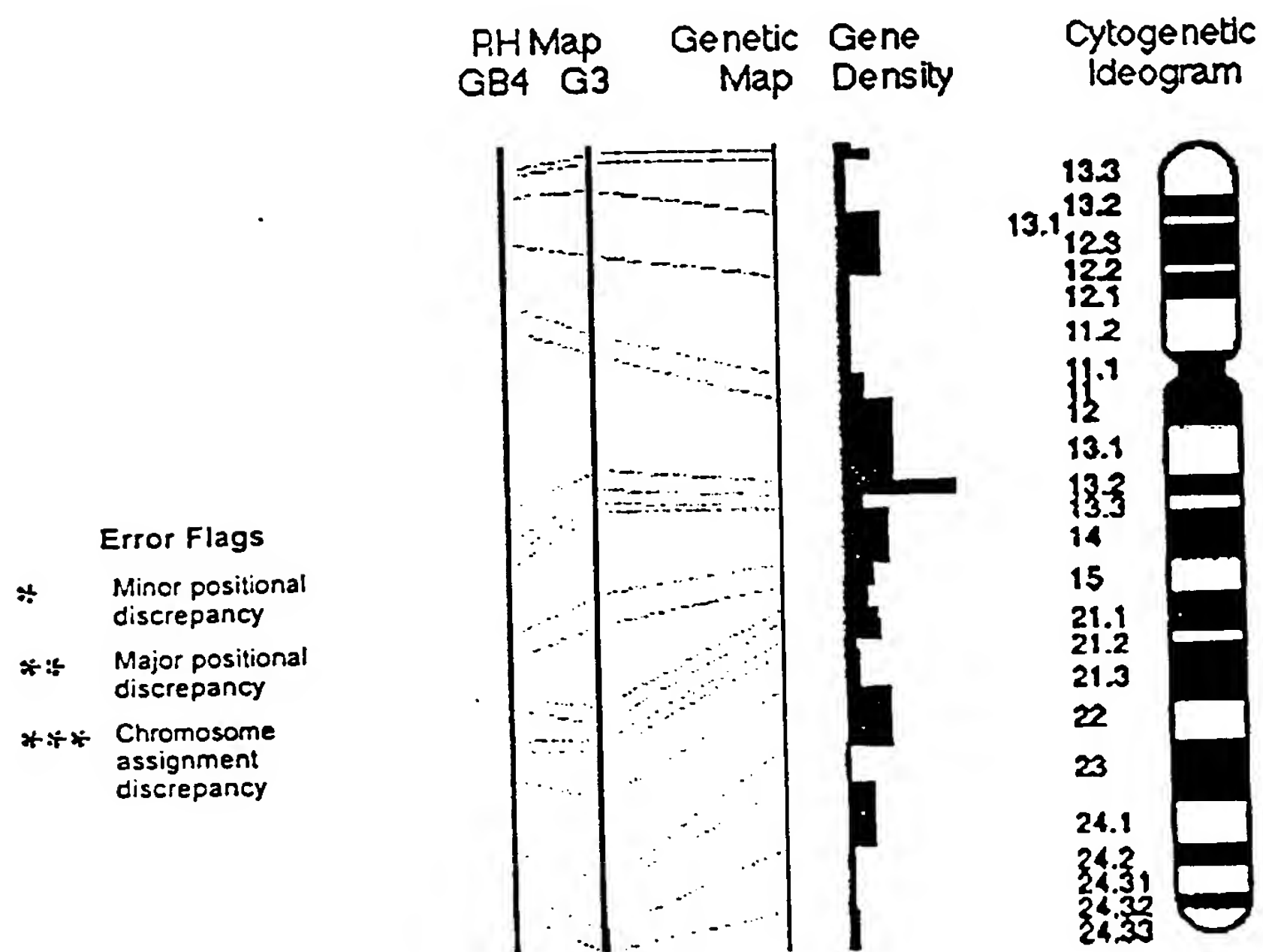
Physical size of bin: 261 cR10000

FIG. 3 C

	↑ Next interval up			
133.8	◆ 5018 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)
135.1	5047 F	AFMa225xe5	D12S1619	Microsatellite marker AFMa225xe5 (SHGC-20..
	◆ 5085 F	SHGC-33949	KIAA0262	KIAA0262 gene product
	◆ 5089 F	SHGC-10488	KIAA0152	KIAA0152 gene product
	◆ 5093 F	SHGC-10346		Homo sapiens HSPC004 mRNA, complete cds
	◆ 5098 F	SHGC-13898		Homo sapiens HSPC004 mRNA, complete cds
137.5	◆ 5163 F	AFM220zf4	D12S321	Microsatellite marker AFM220zf4 (SHGC-212..
	5199 F	SHGC-11702		ESTs
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)
	↓ Next interval down			

FIG. 3 D

## Chromosome 12: D12S340-D12S97



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

### About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

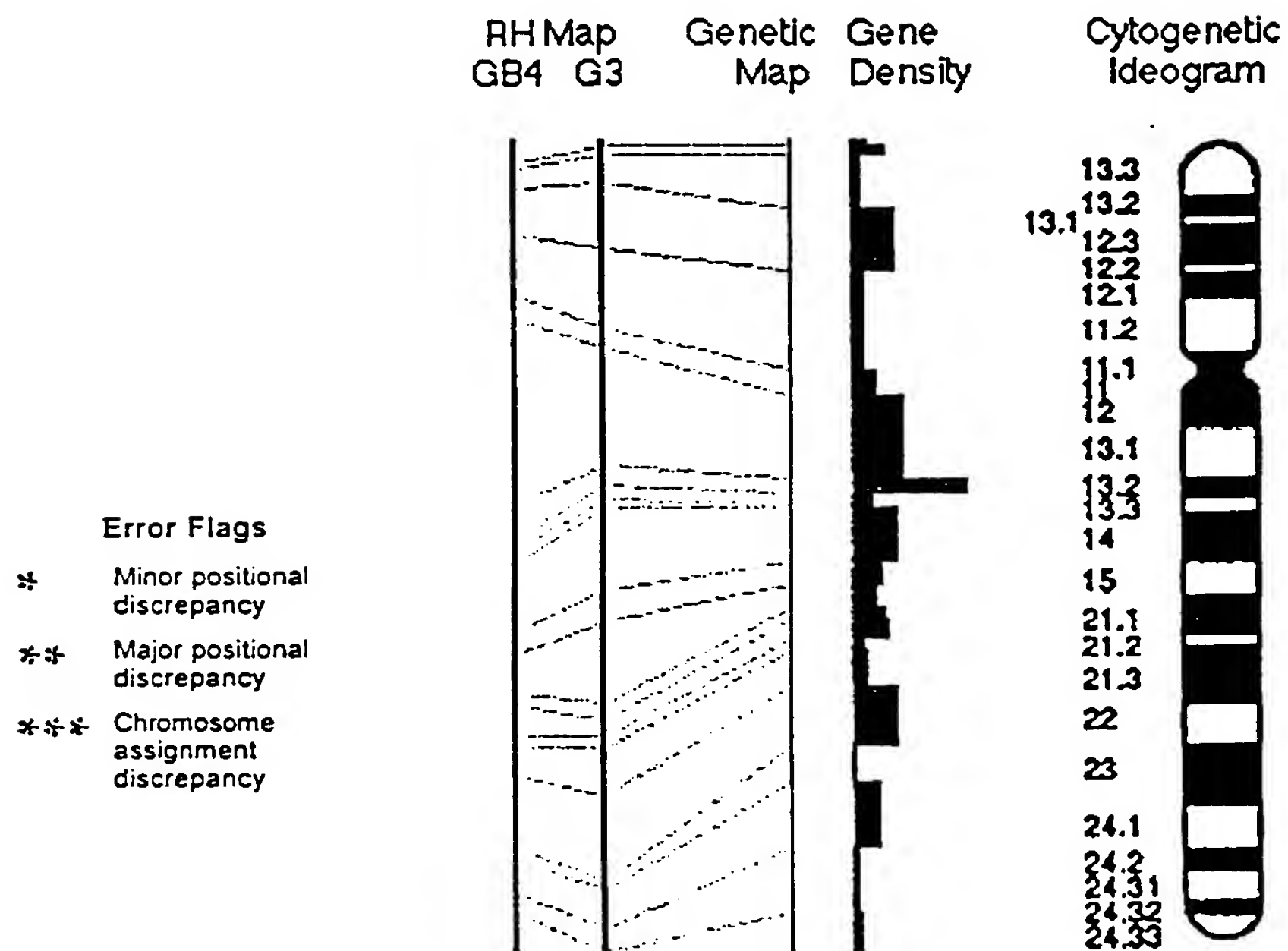
Physical size of bin: 151 cR10000

FIG. 3 E

					Next interval up
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)	
148.3	5288 F	AFM234tb10	D12S324	Microsatellite marker AFM234tb10 (SHGC-21..	
154.4	5316 F	AFMb350zb5	D12S1679	Microsatellite marker AFMb350zb5 (SHGC-20..	
149.5	5358 F	AFM198wh2	D12S307	Microsatellite marker AFM198wh2 (SHGC-211..	
157.2	5393 F	AFMb301we5	D12S1659	Microsatellite marker AFMb301we5 (SHGC-20..	
160.9	◆ 5415 F	AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1 (SHGC-21..	
160.9	◆ 5430 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6 (SHGC-372)	

FIG. 3 F

## Chromosome 12: D12S97-qTEL



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

### About This Interval

Top of interval: D12S97 (160.9 cM)

Bottom of interval: chr12\_qTEL (169.1 cM)

Genetic size of bin: 8 cM

Physical size of bin: -4429 cR10000

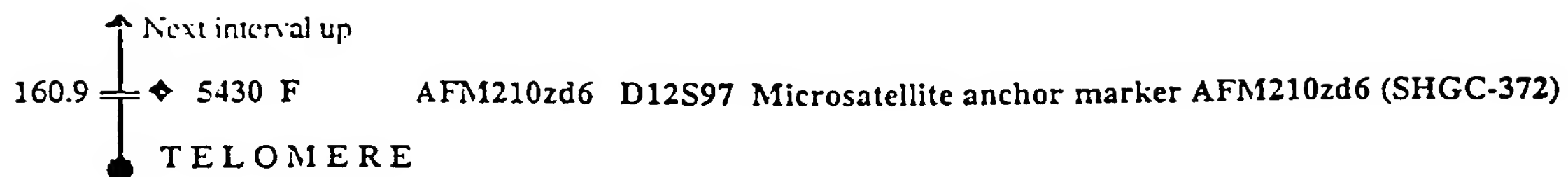


FIG. 3 G

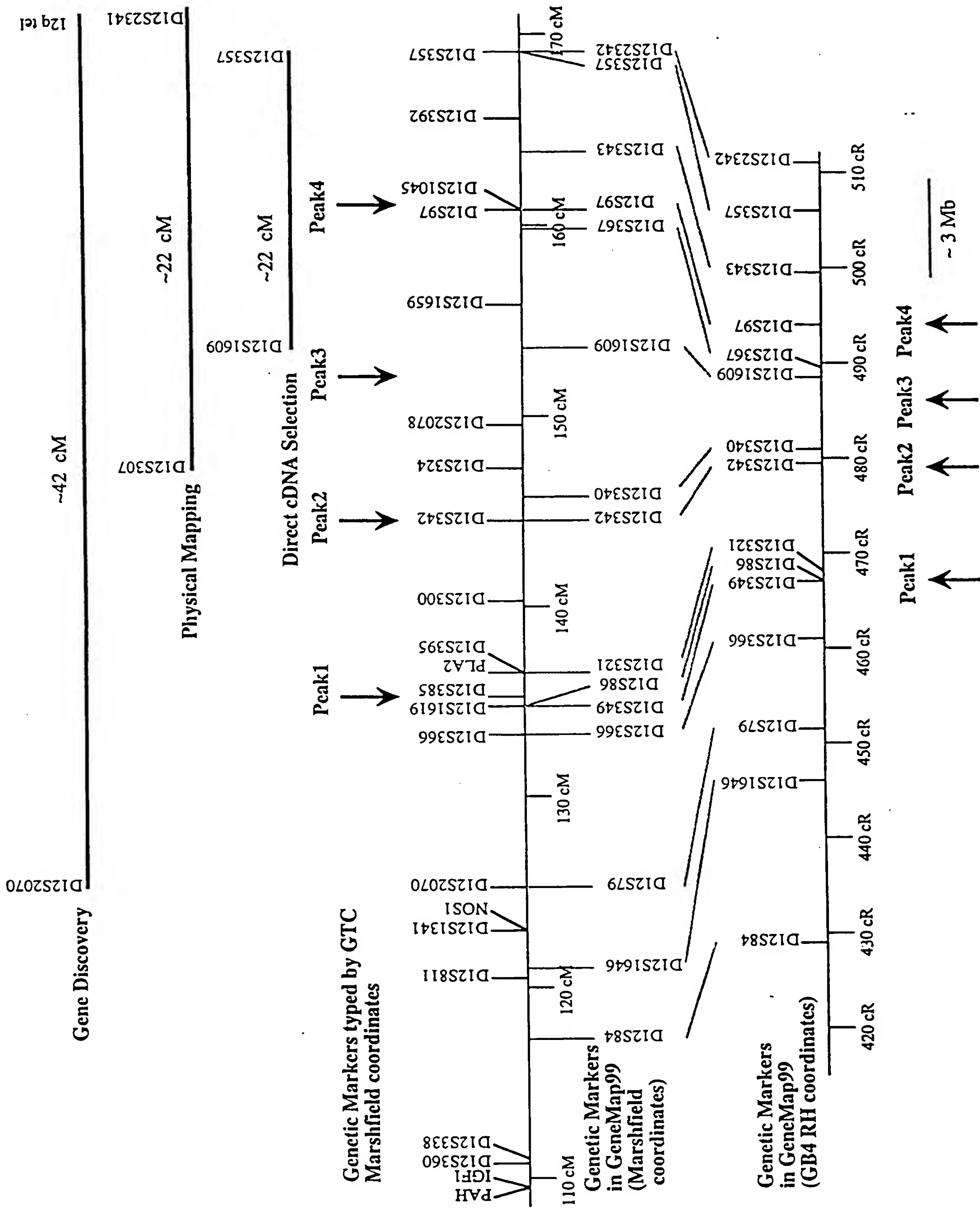


FIG. 4



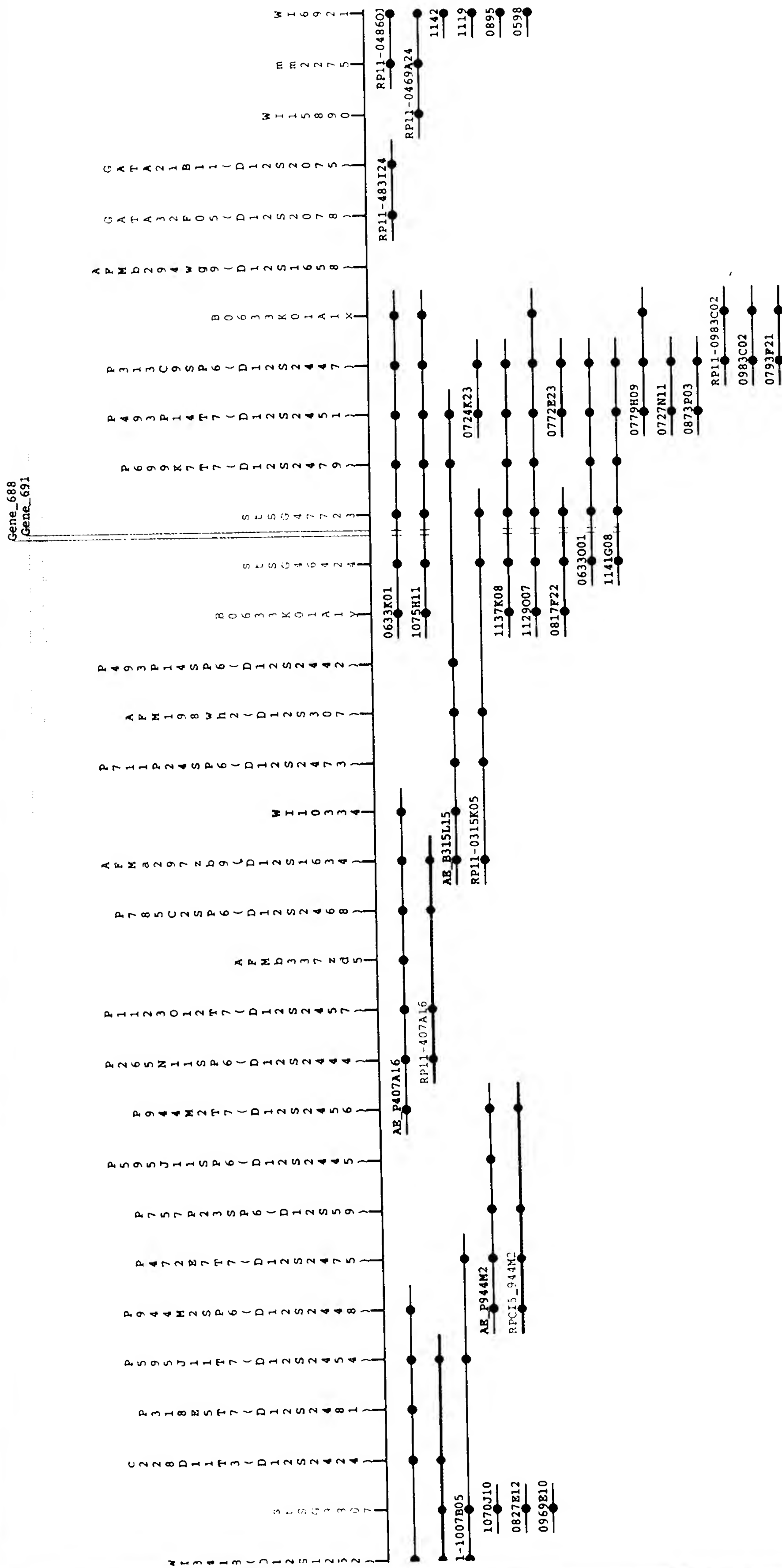
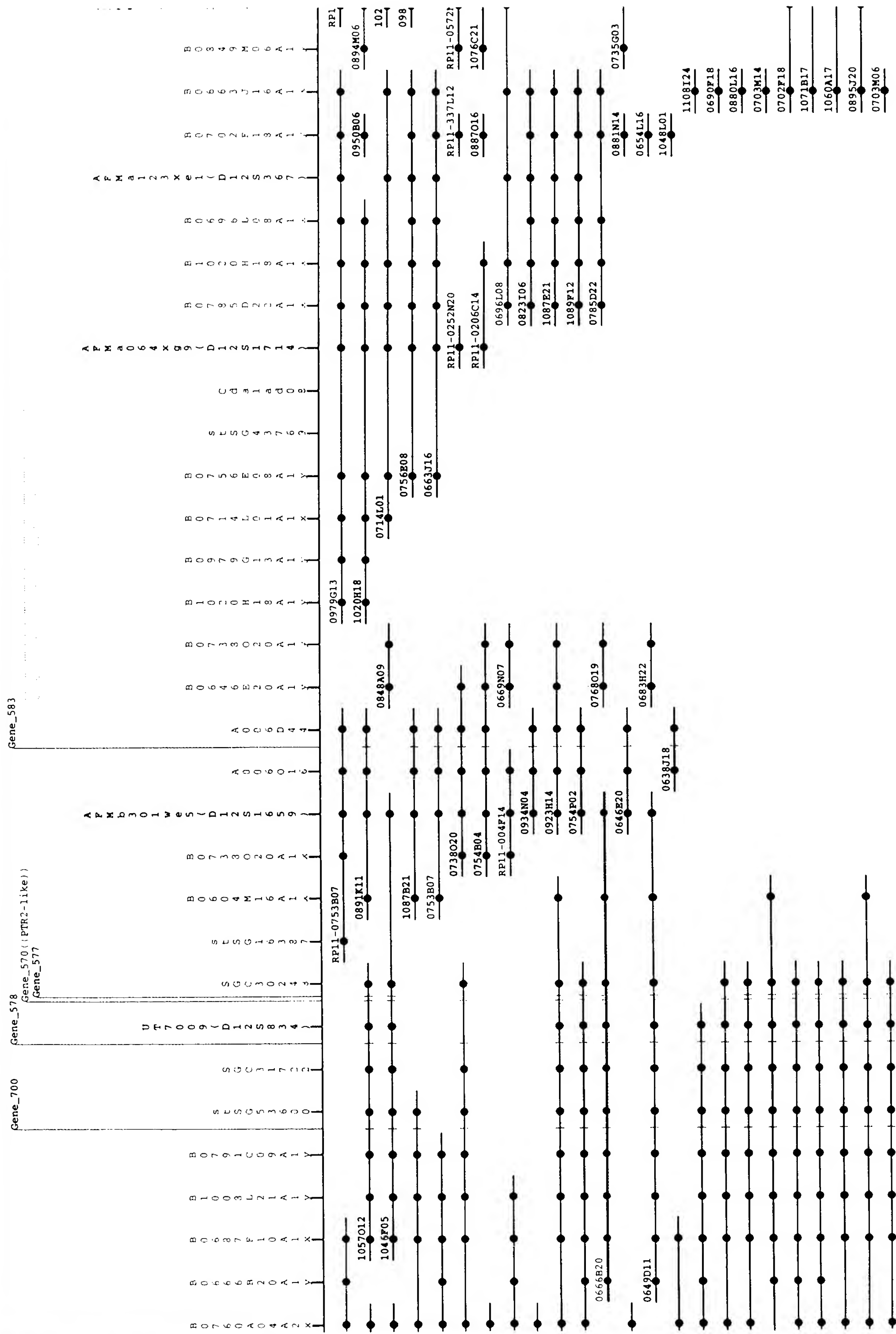
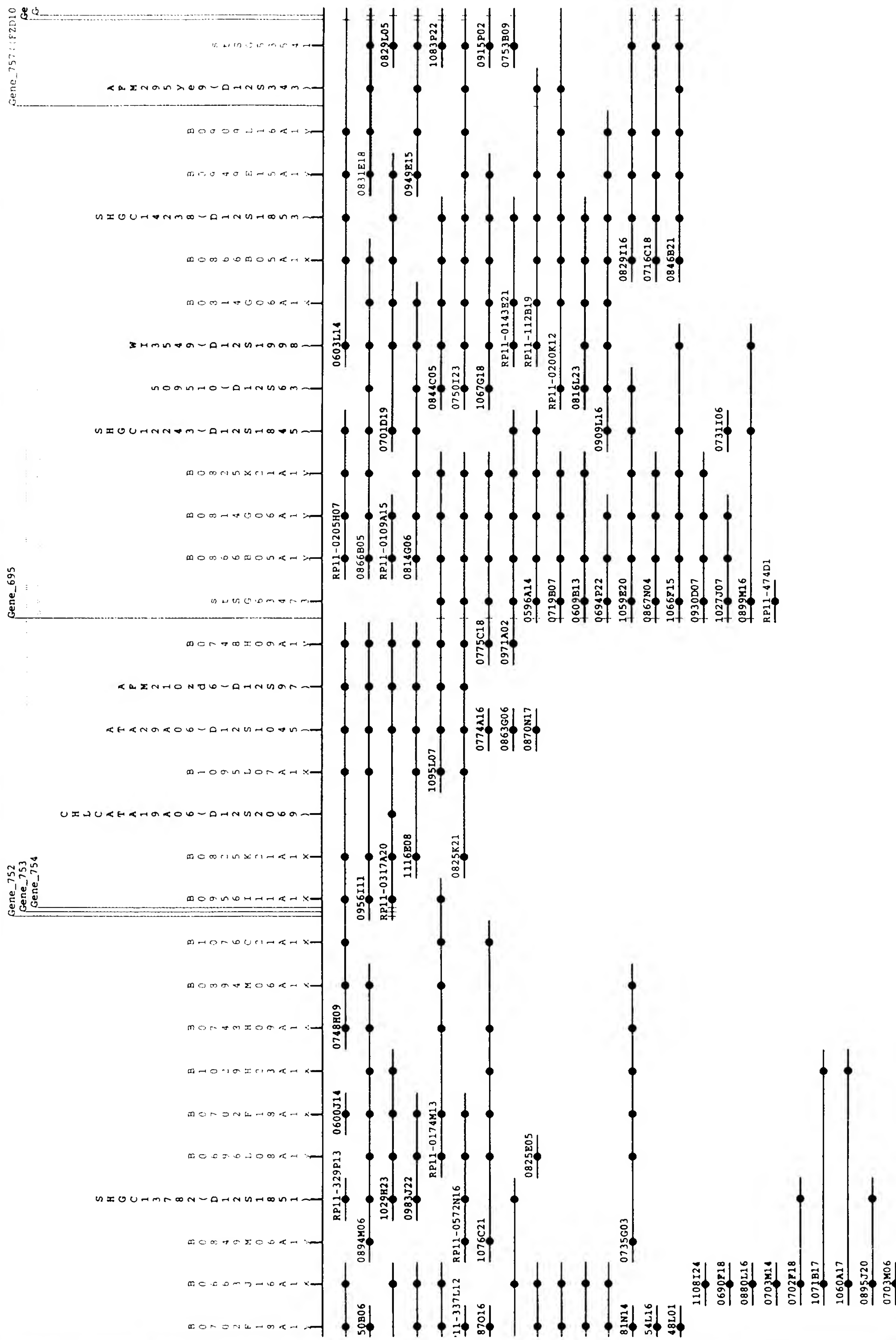


FIG. 5A





**FIG. 5C**



**FIG. 5D**

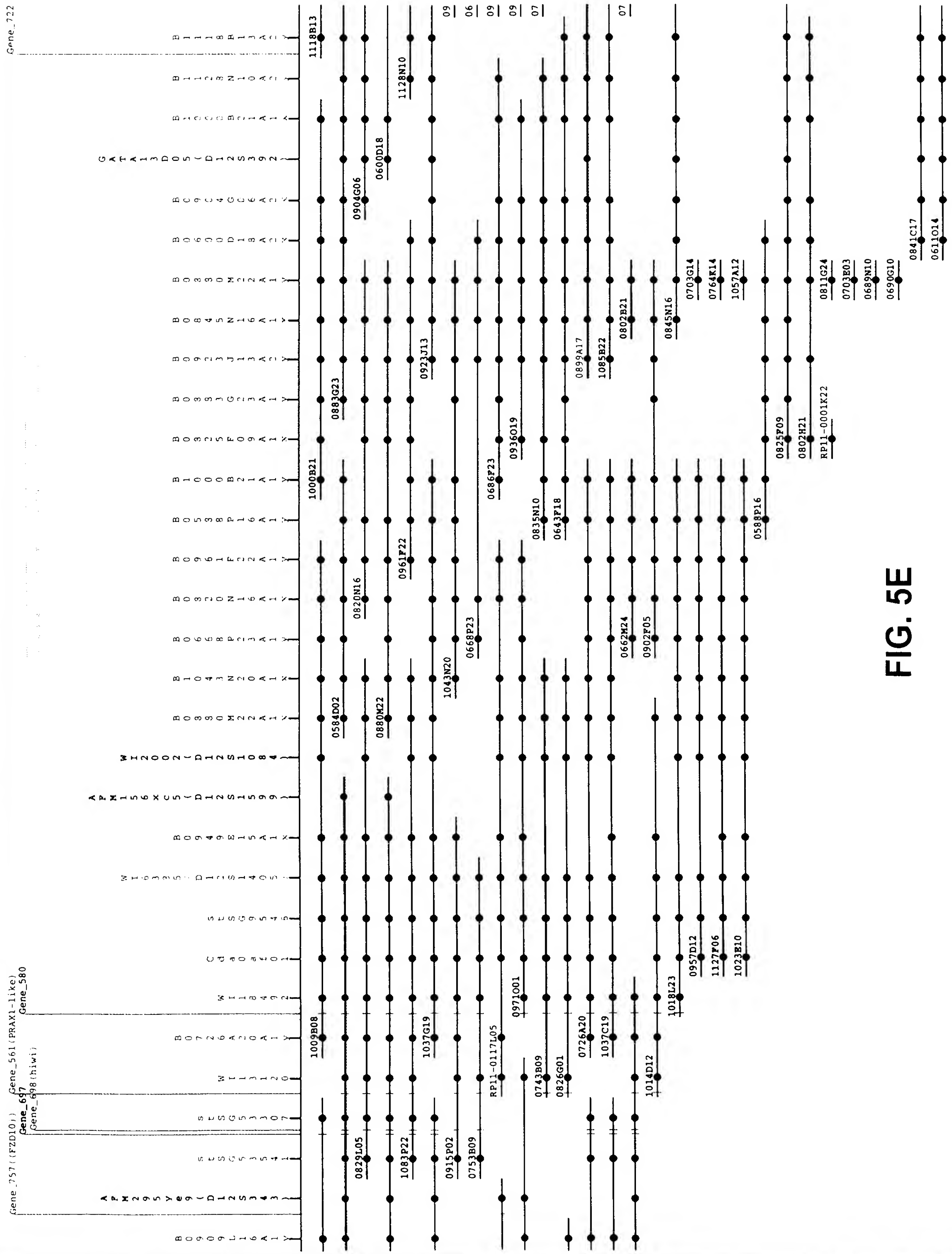
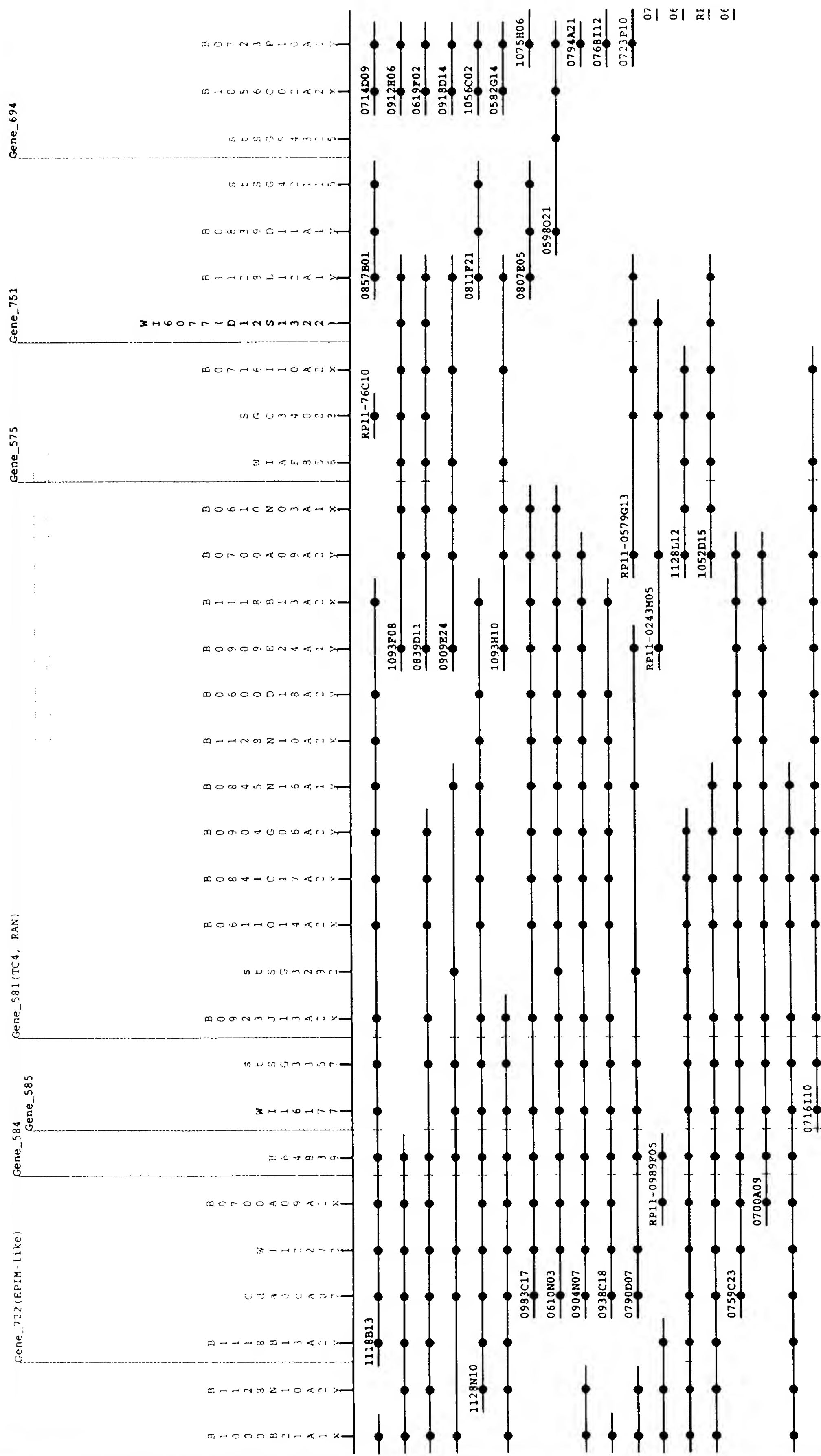
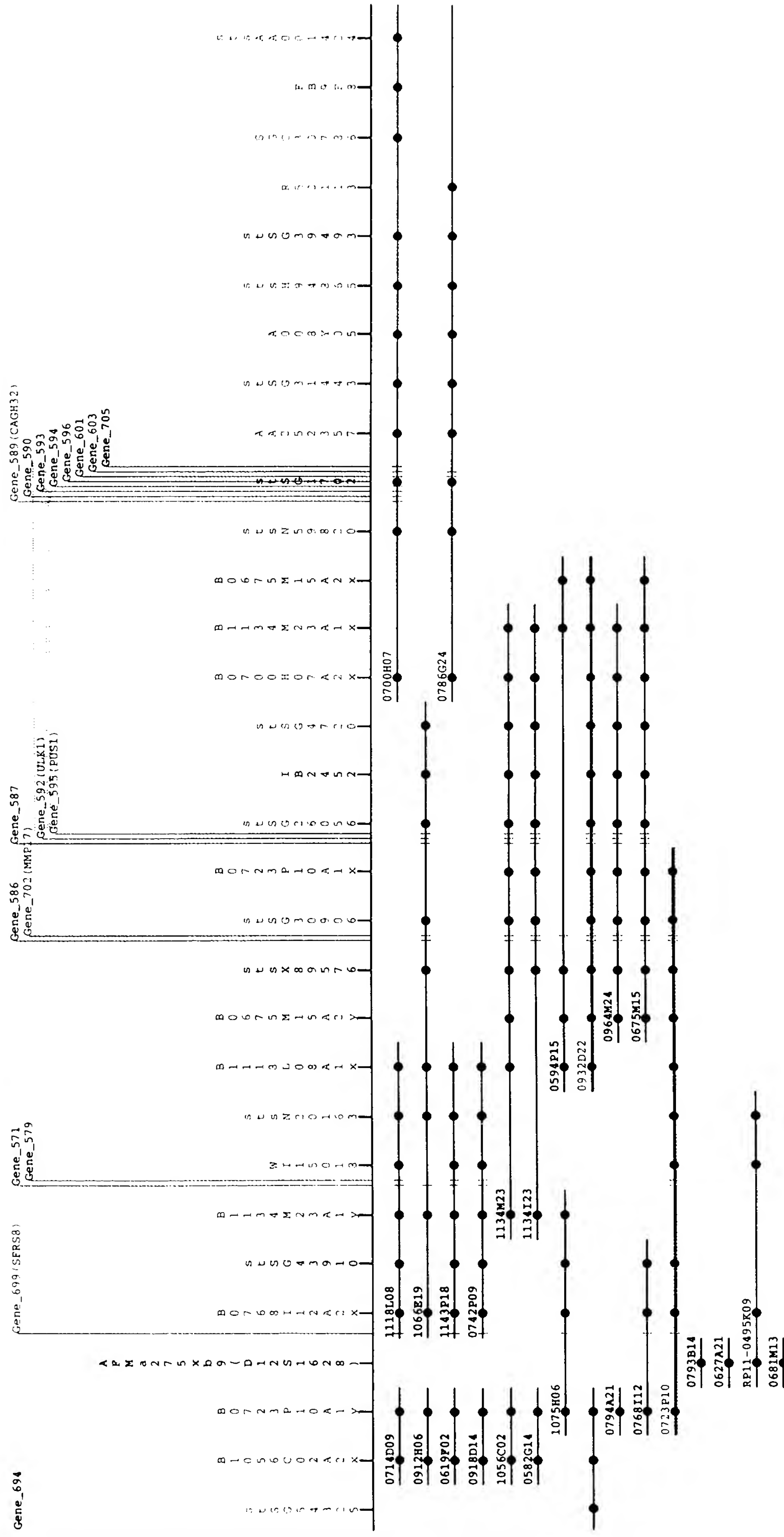


FIG. 5E



**FIG. 5F**





**FIG. 5G**

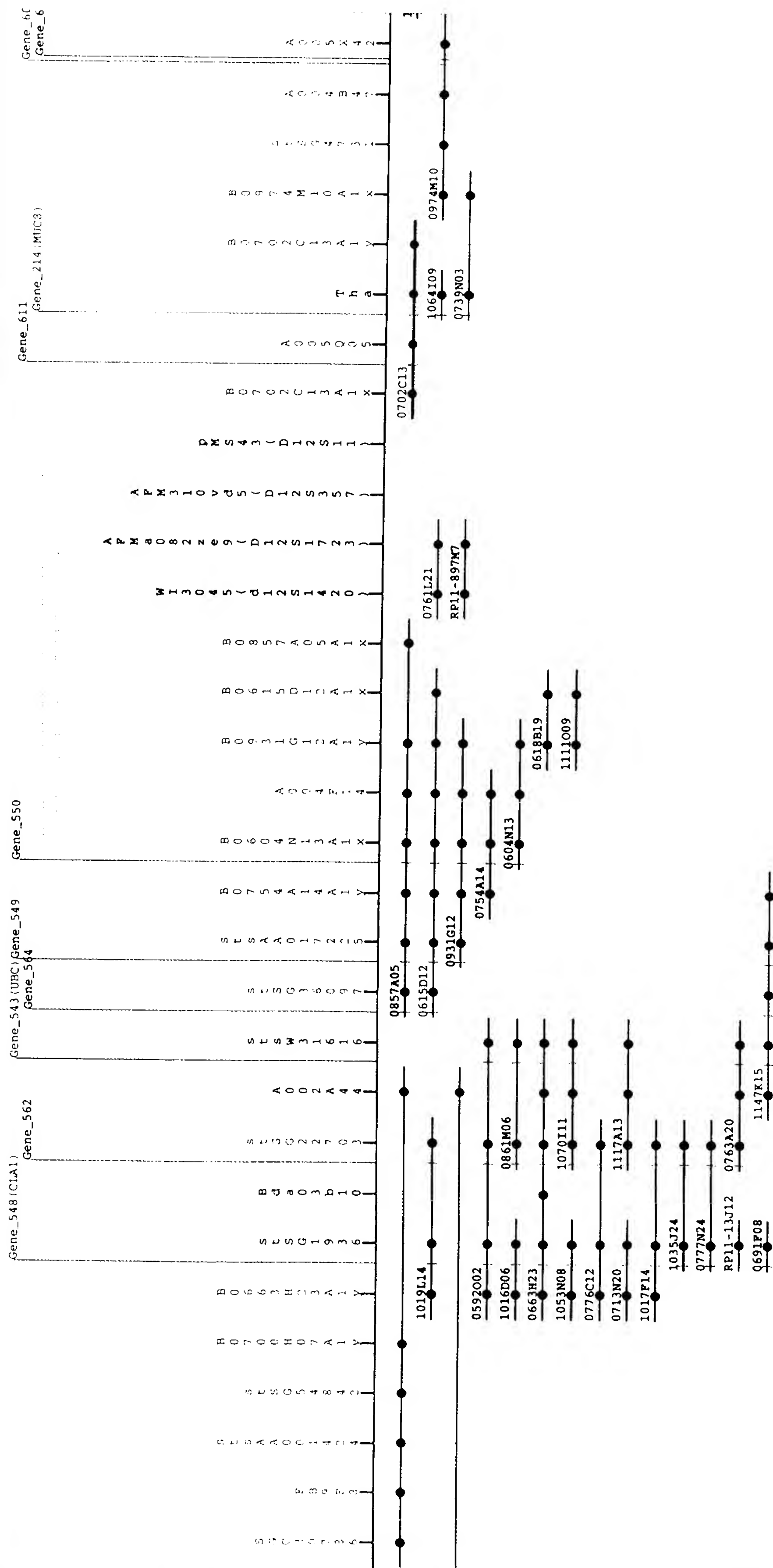
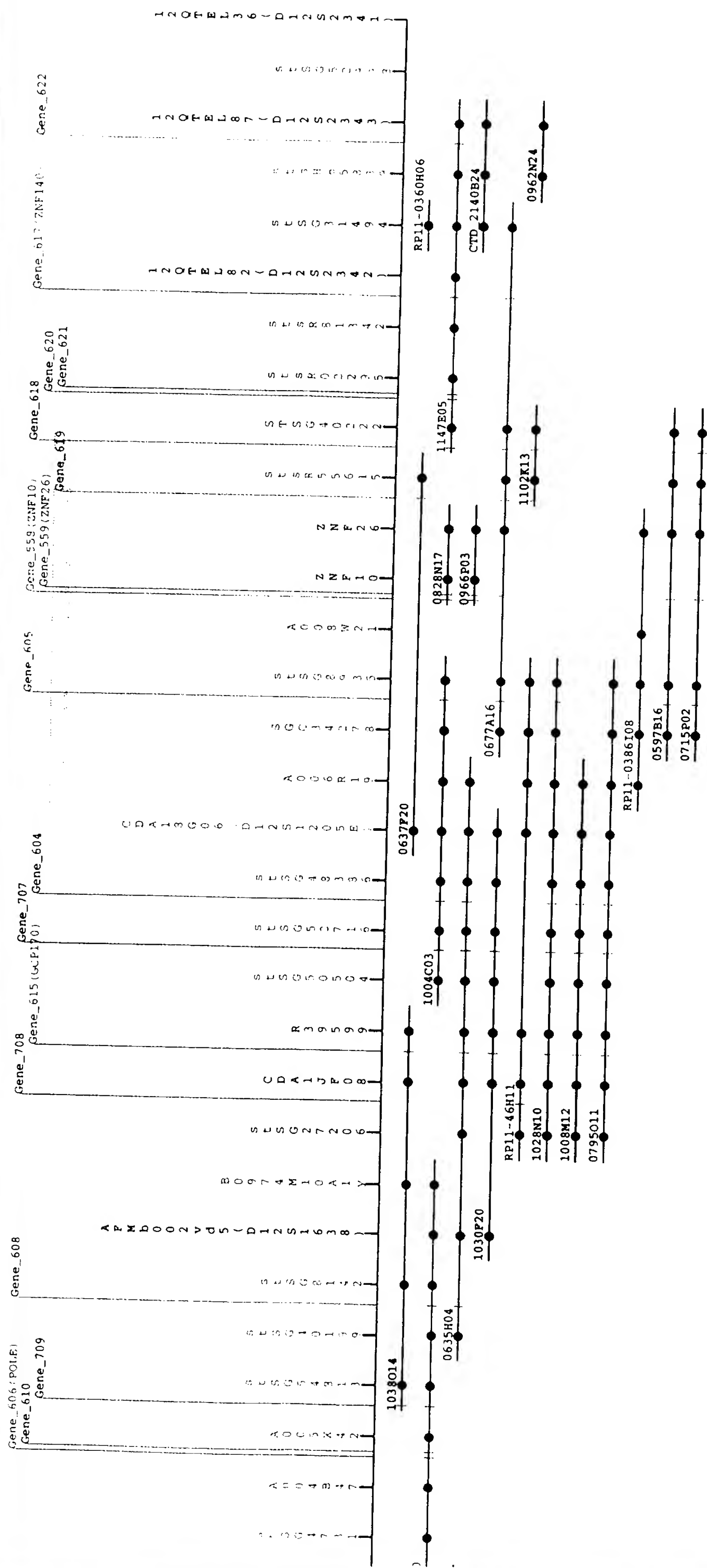


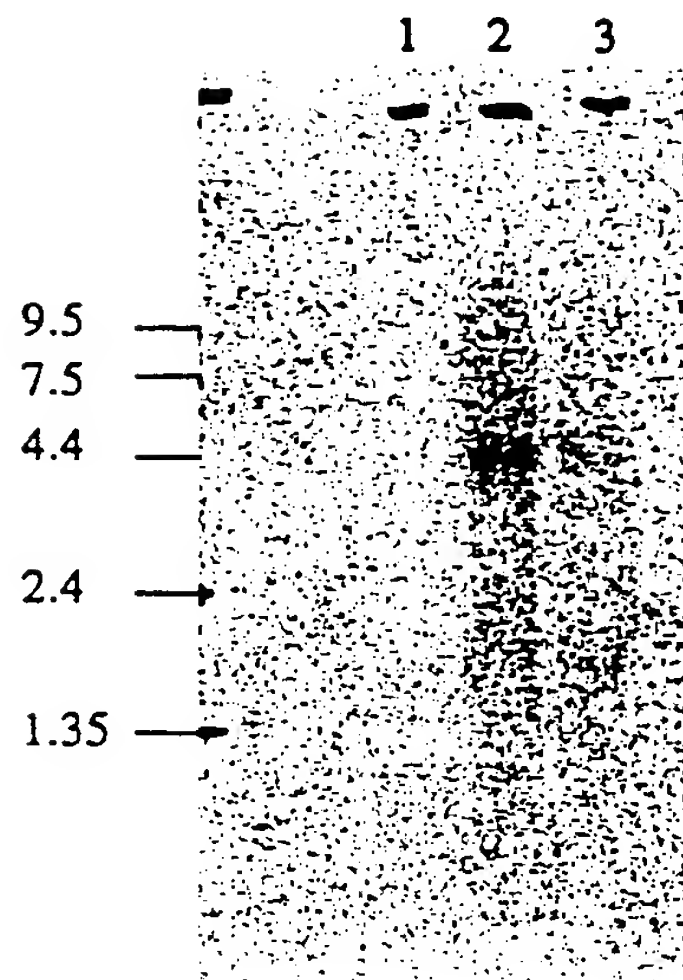
FIG. 5H





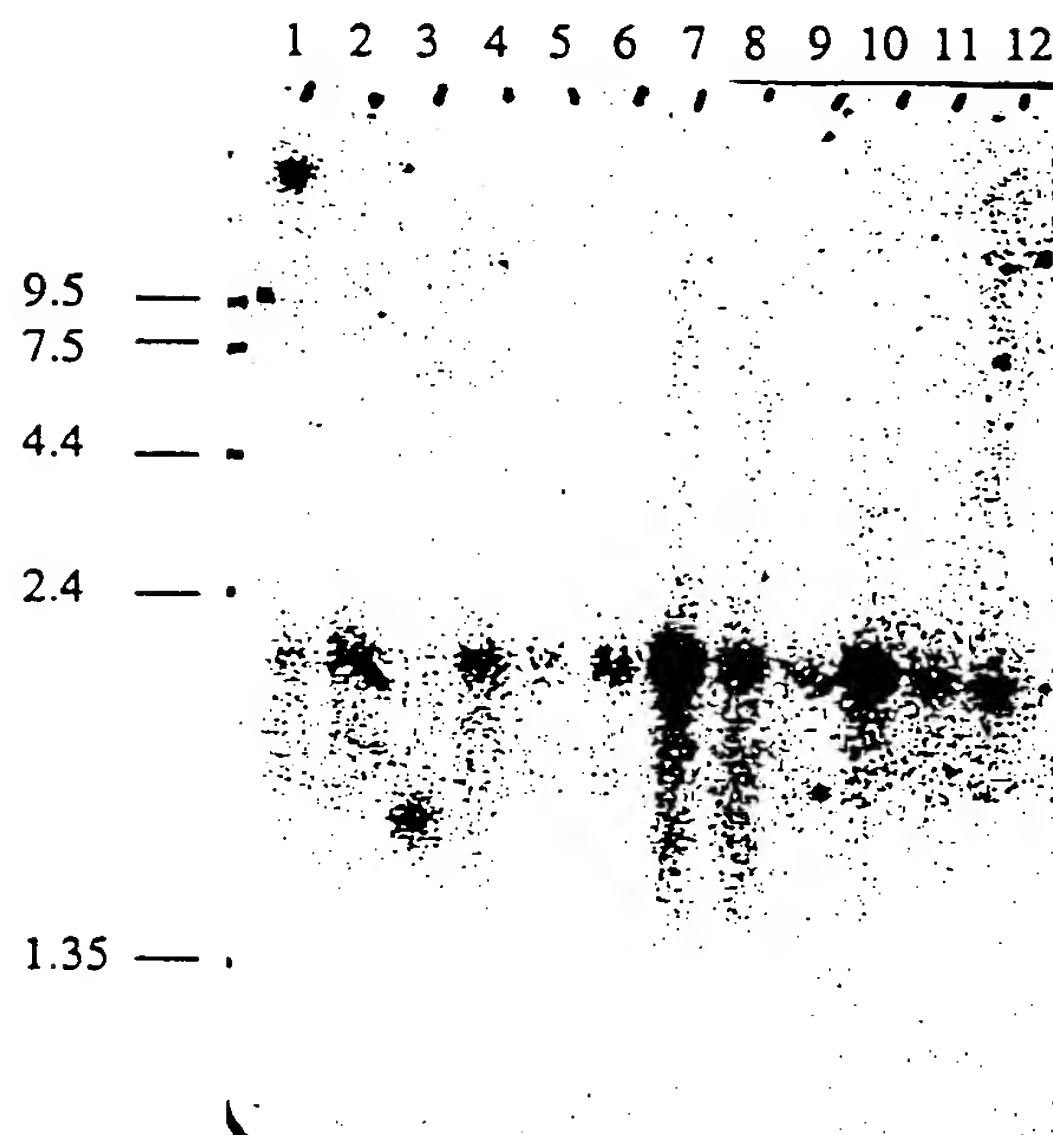
**FIG. 51**

# Gene 214



- 1. Lymphoblastoid cell line
- 2. Lung
- 3. Trachea

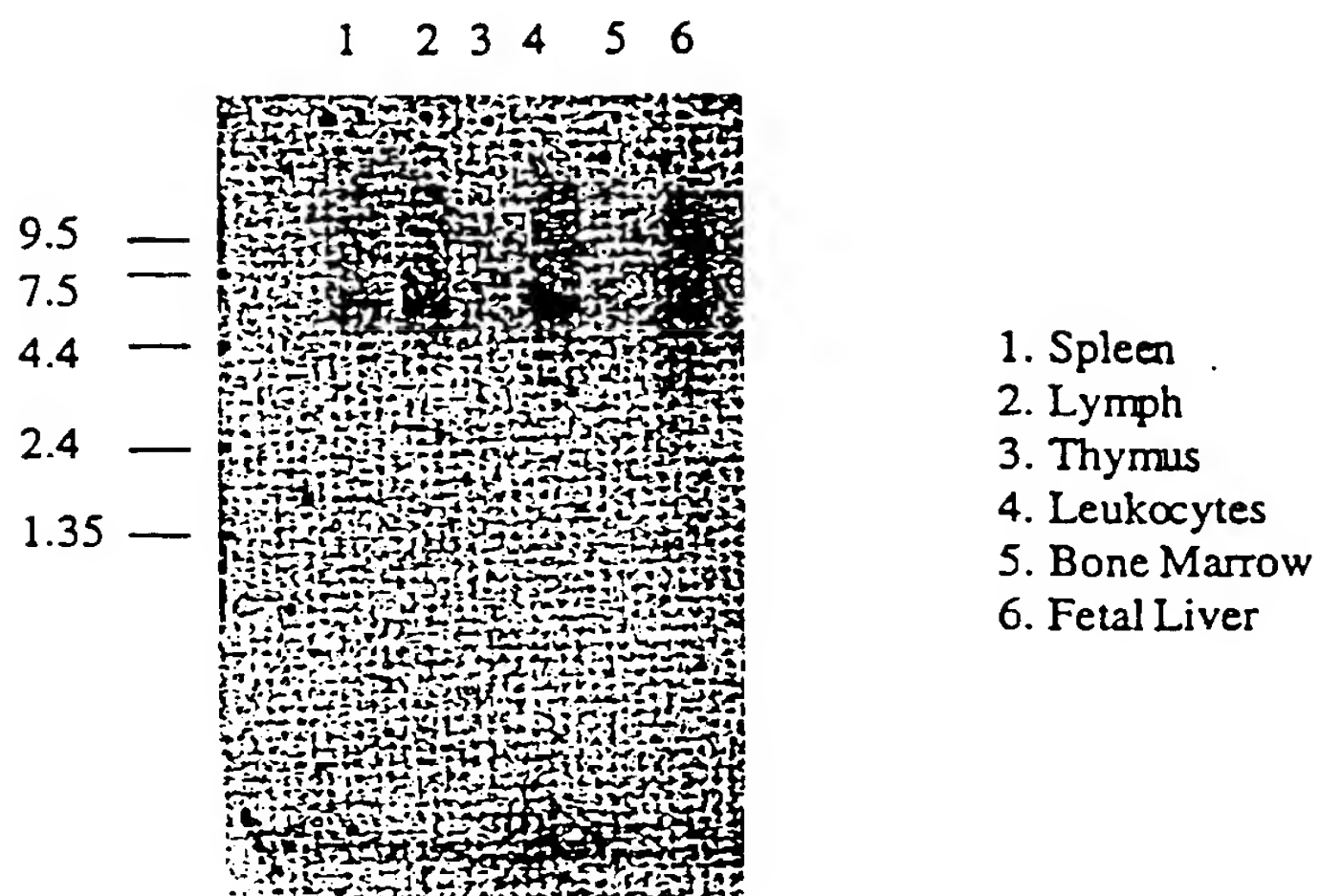
# Gene 436



- 1. Brain
- 2. Heart
- 3. Skeletal Muscle
- 4. Colon
- 5. Thymus
- 6. Spleen
- 7. Kidney
- 8. Liver
- 9. Small Intestine
- 10. Placenta
- 11. Lung
- 12. Leukocytes

FIG. 6 A

# Gene 454



# Gene 515

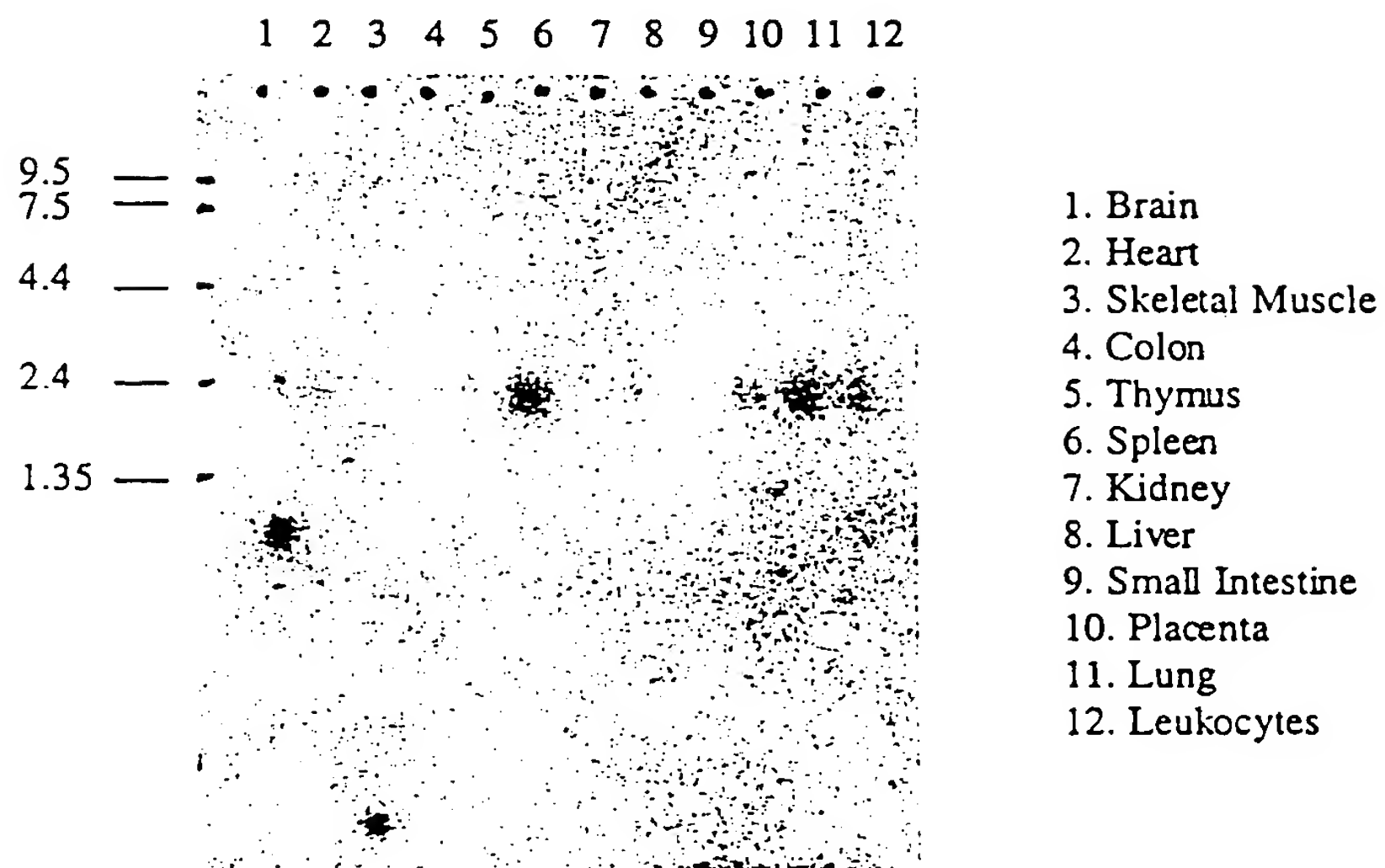
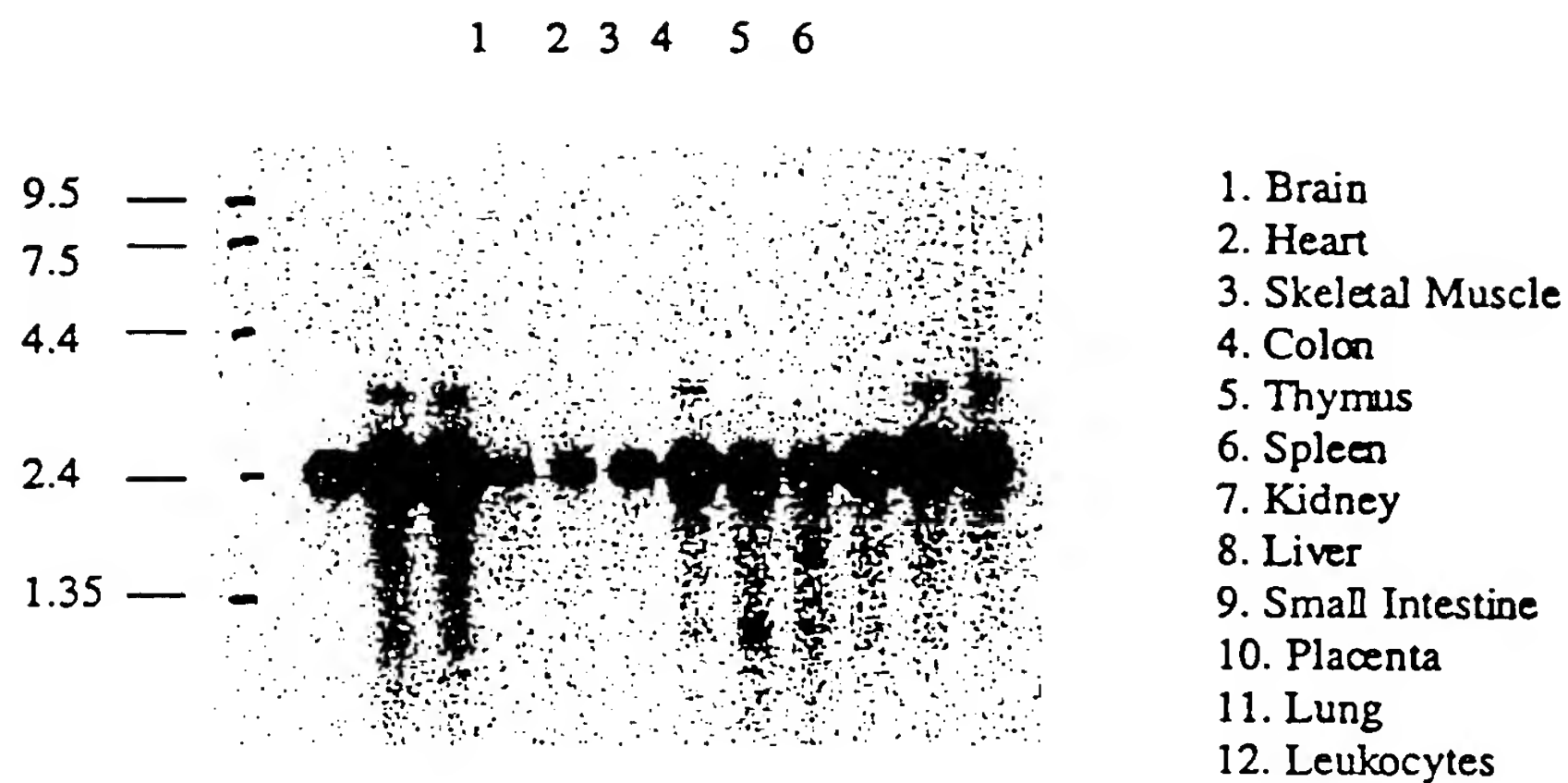


FIG. 6 B

# Gene 543



# Gene 548

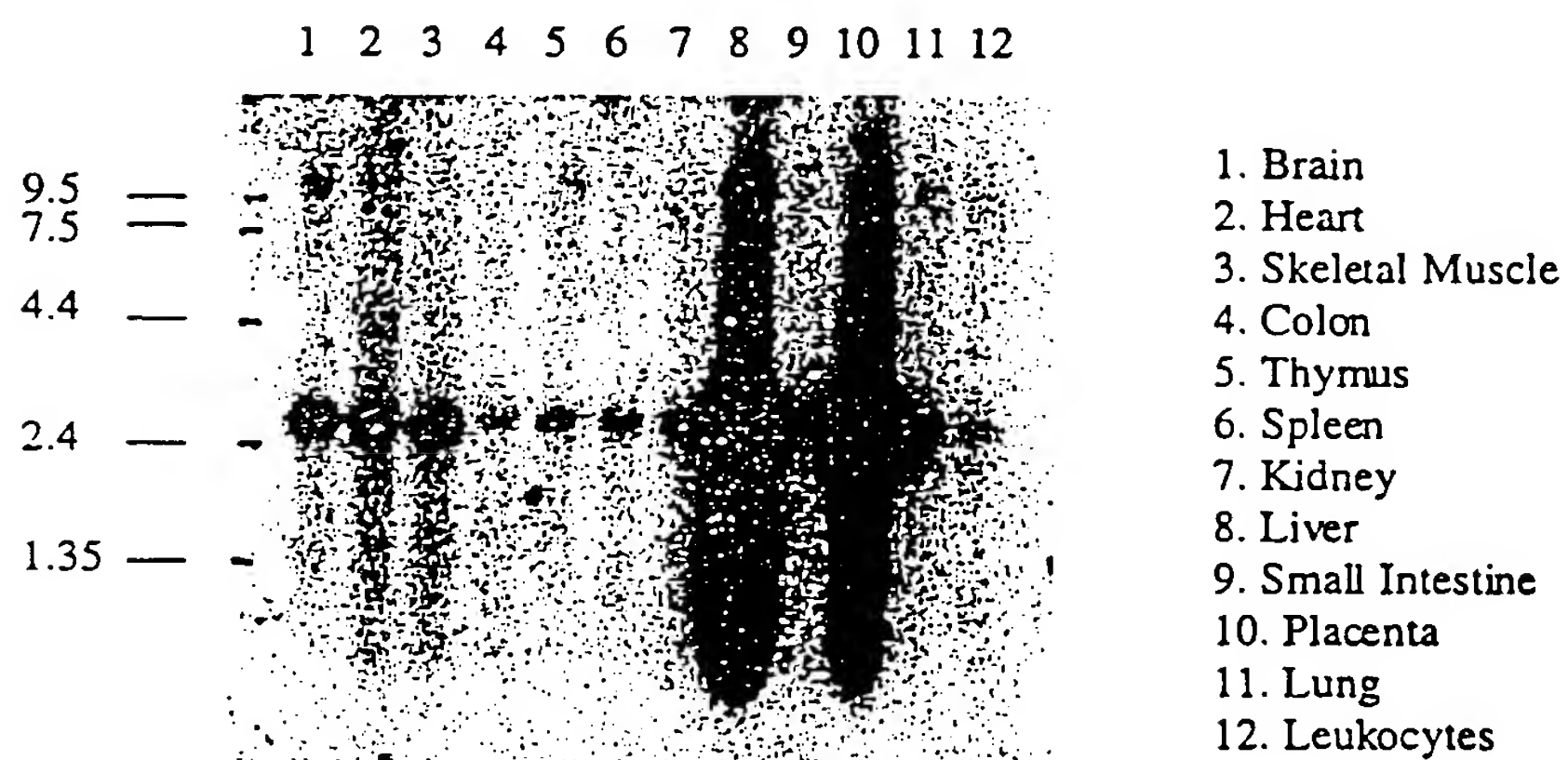
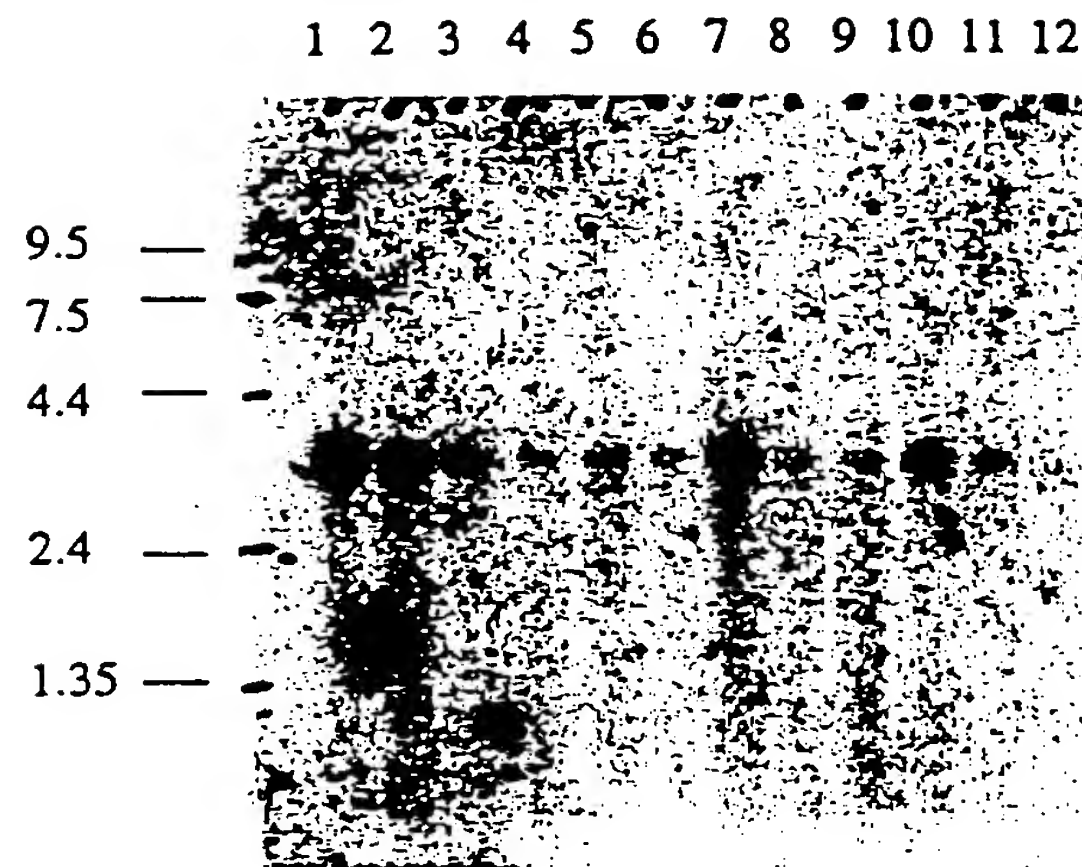


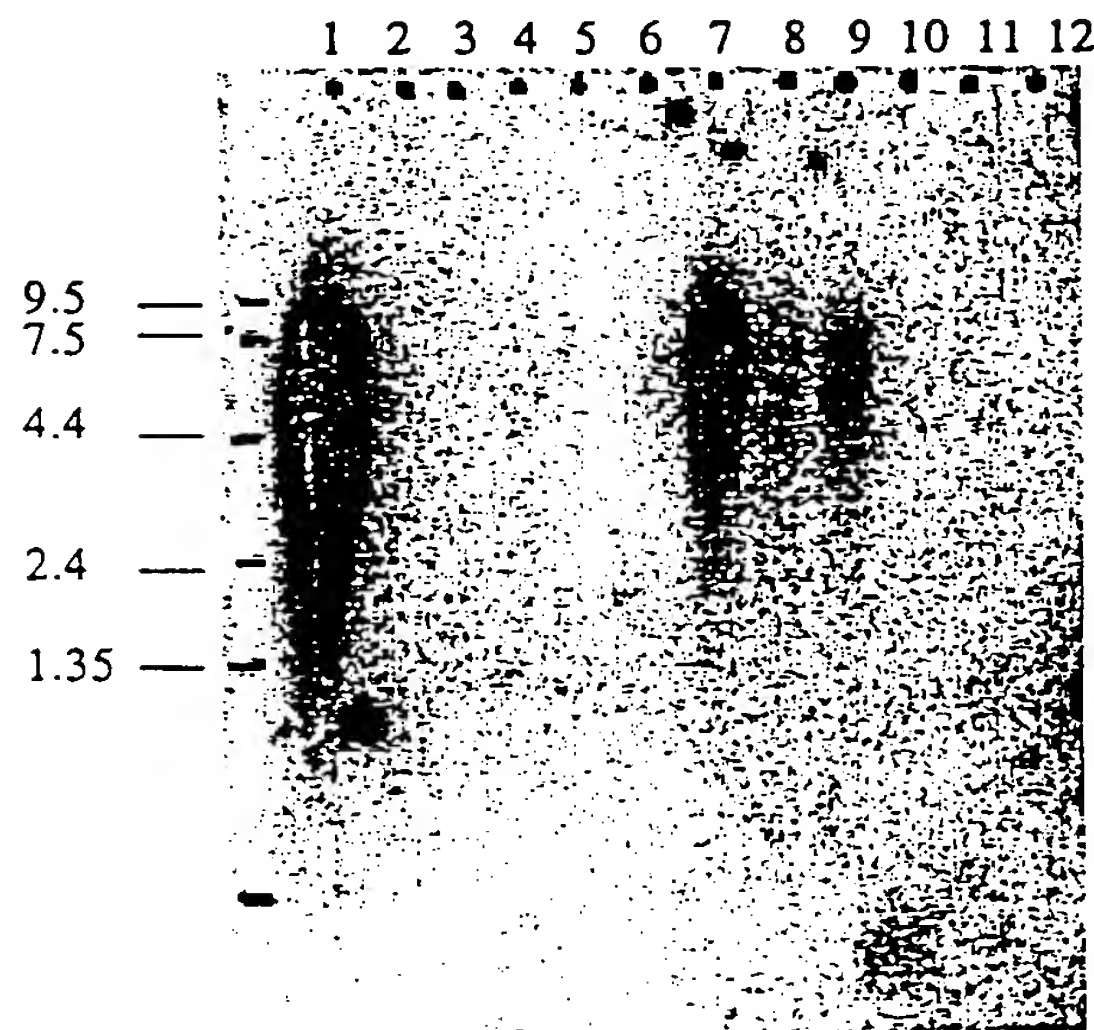
FIG. 6 C

# Gene 550



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

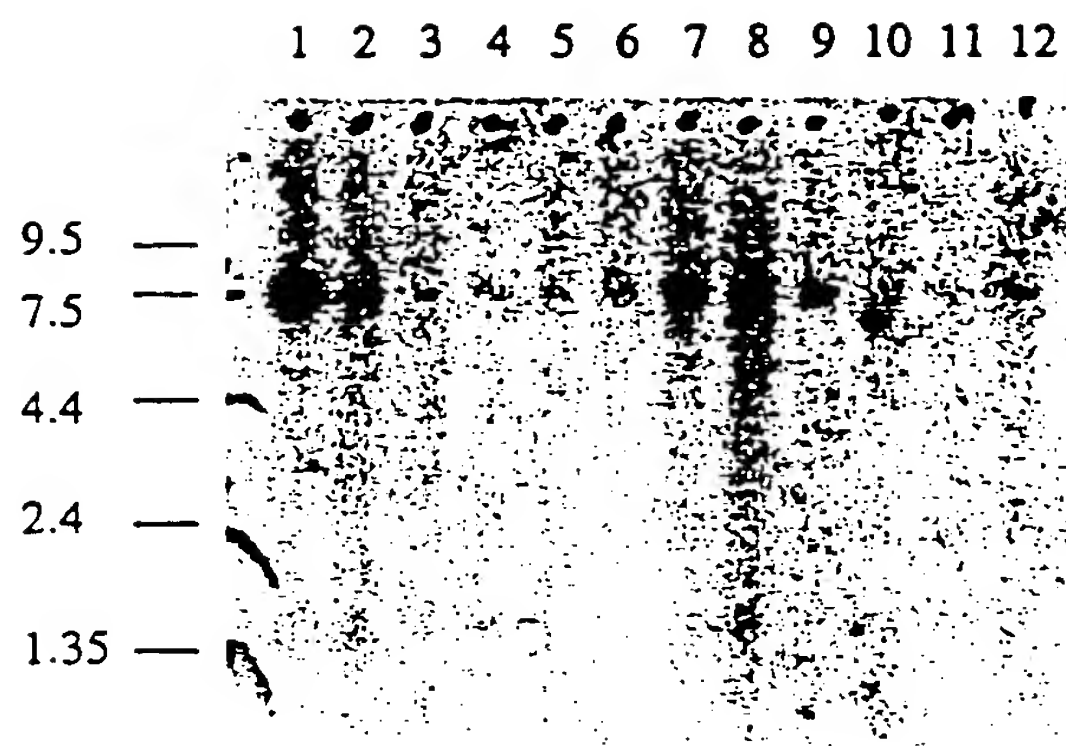
# Gene 561



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

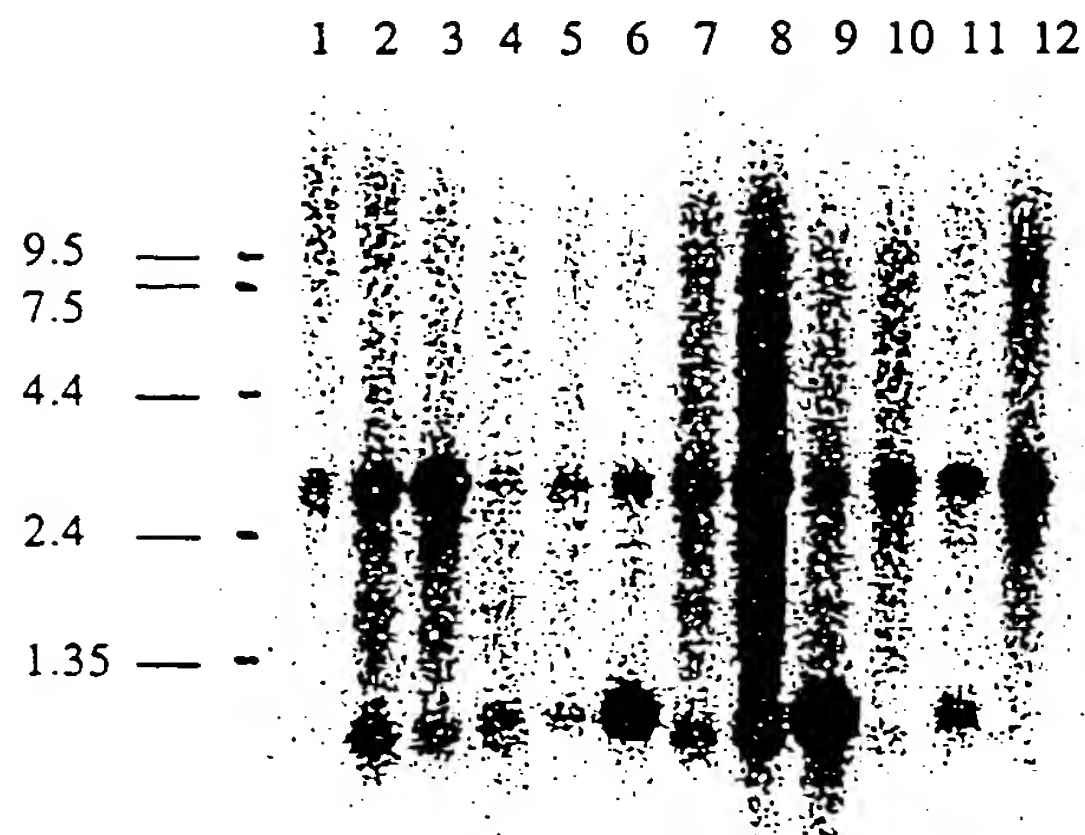
FIG. 6 D

# Gene 564



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

# Gene 570

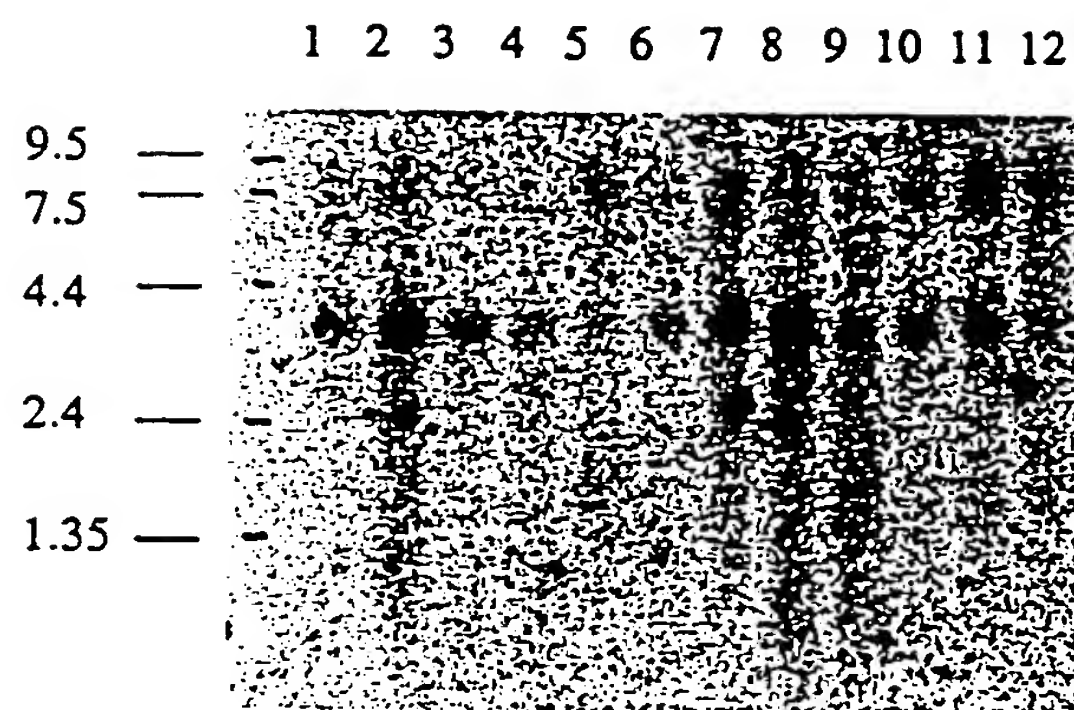


1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 E

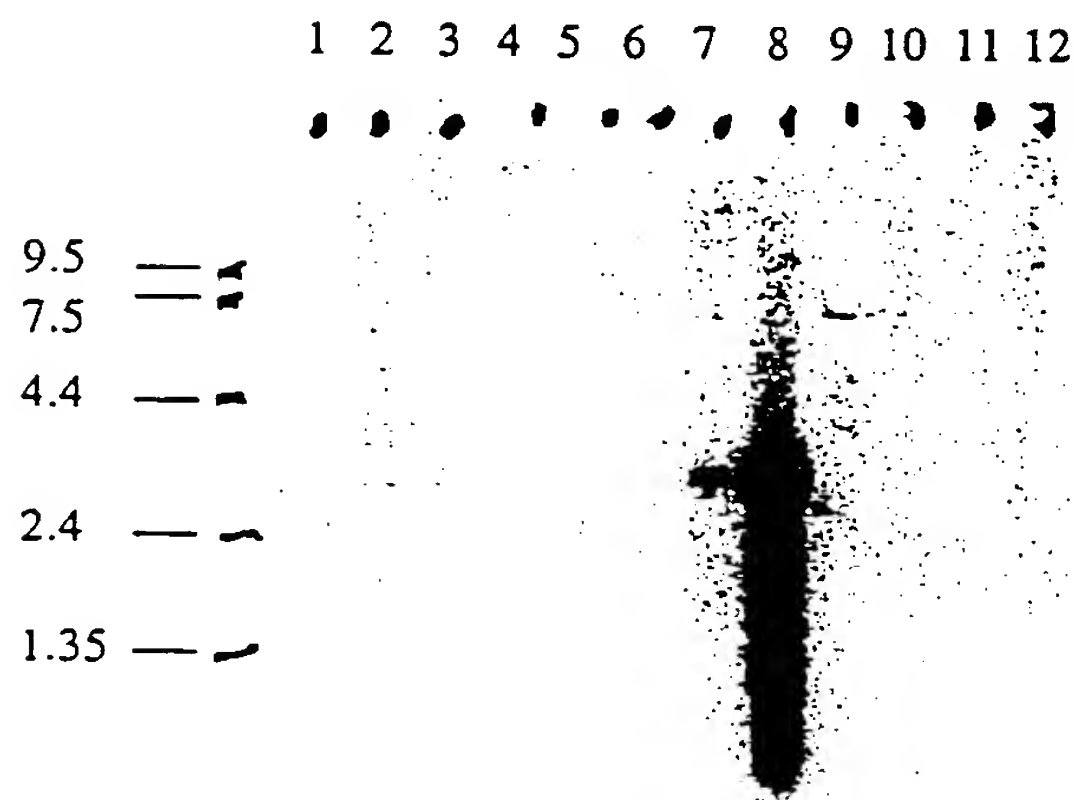


# Gene 576



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

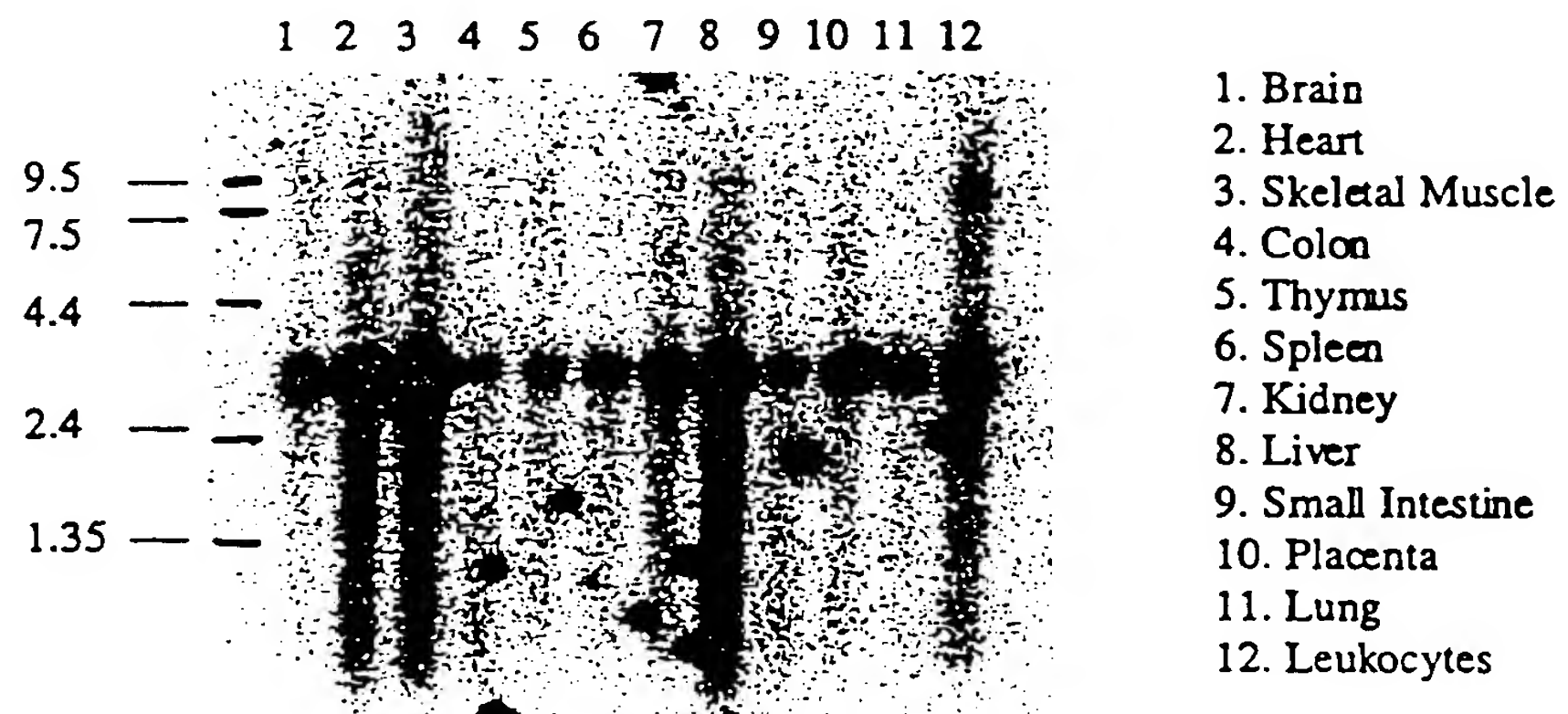
# Gene 577



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 F

# Gene 578



# Gene 579

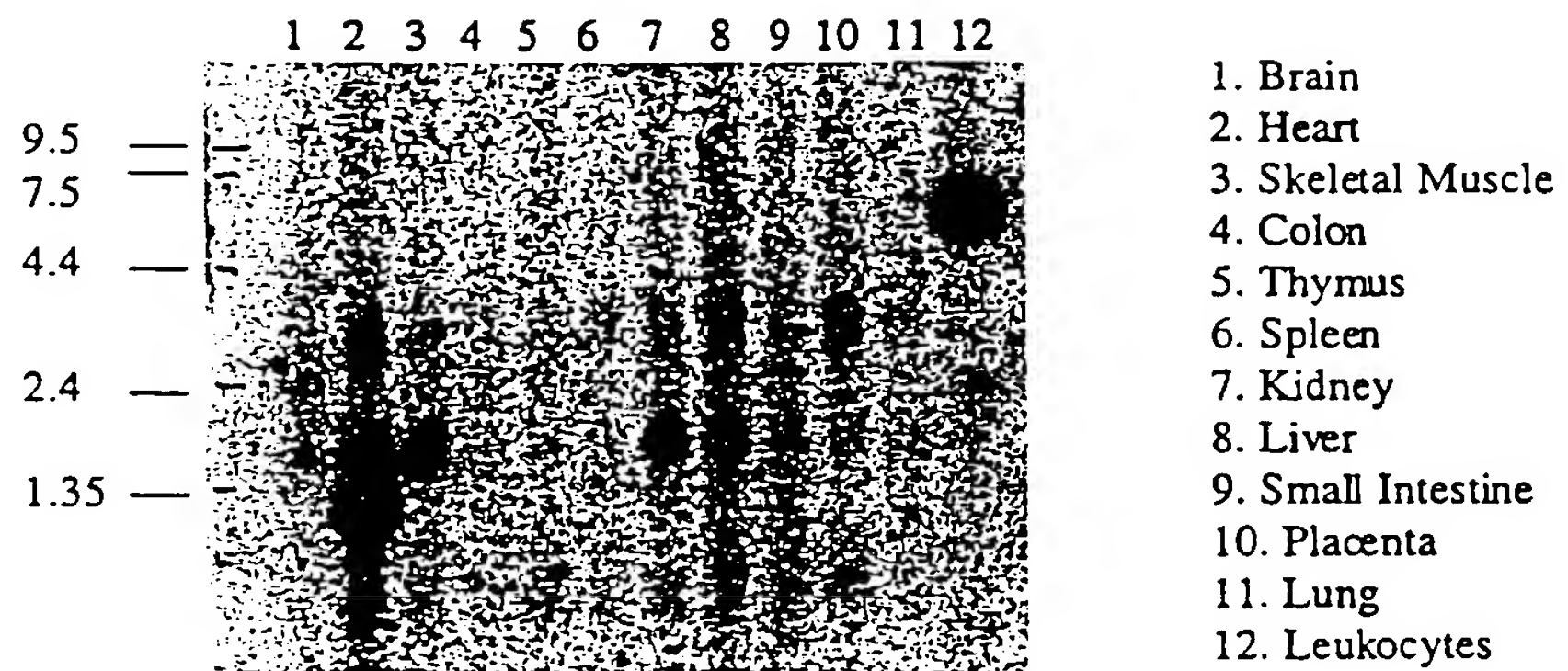
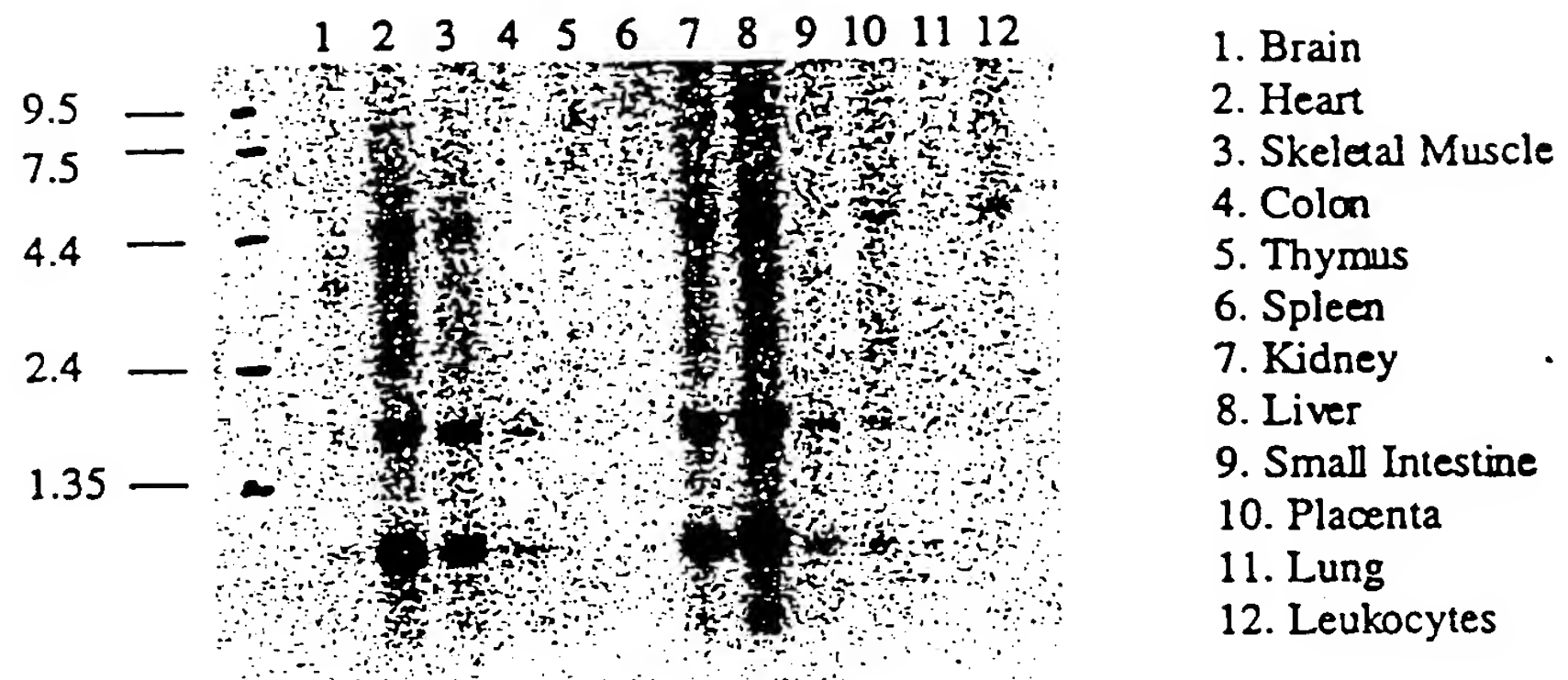


FIG. 6 G



# Gene 580



# Gene 581

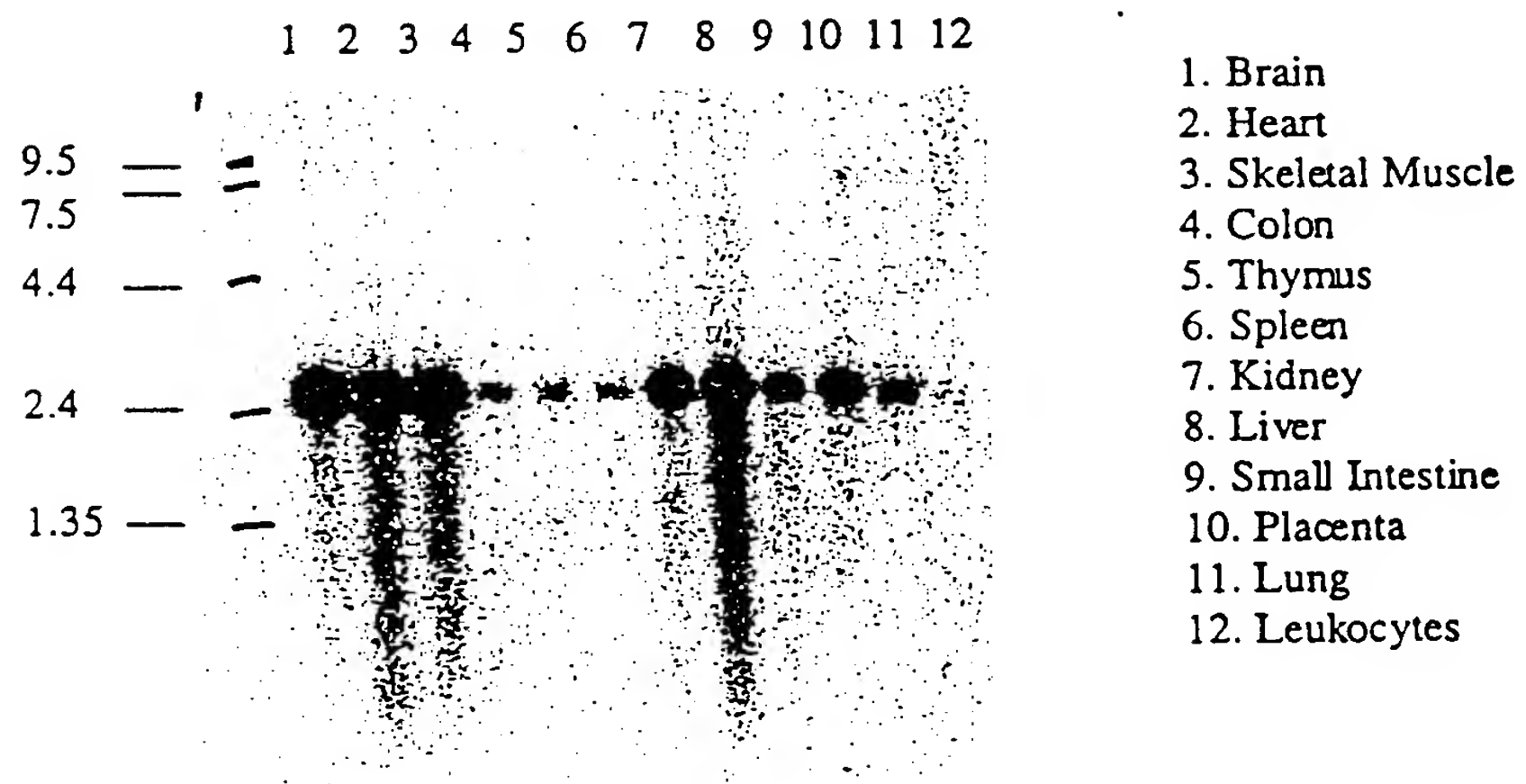
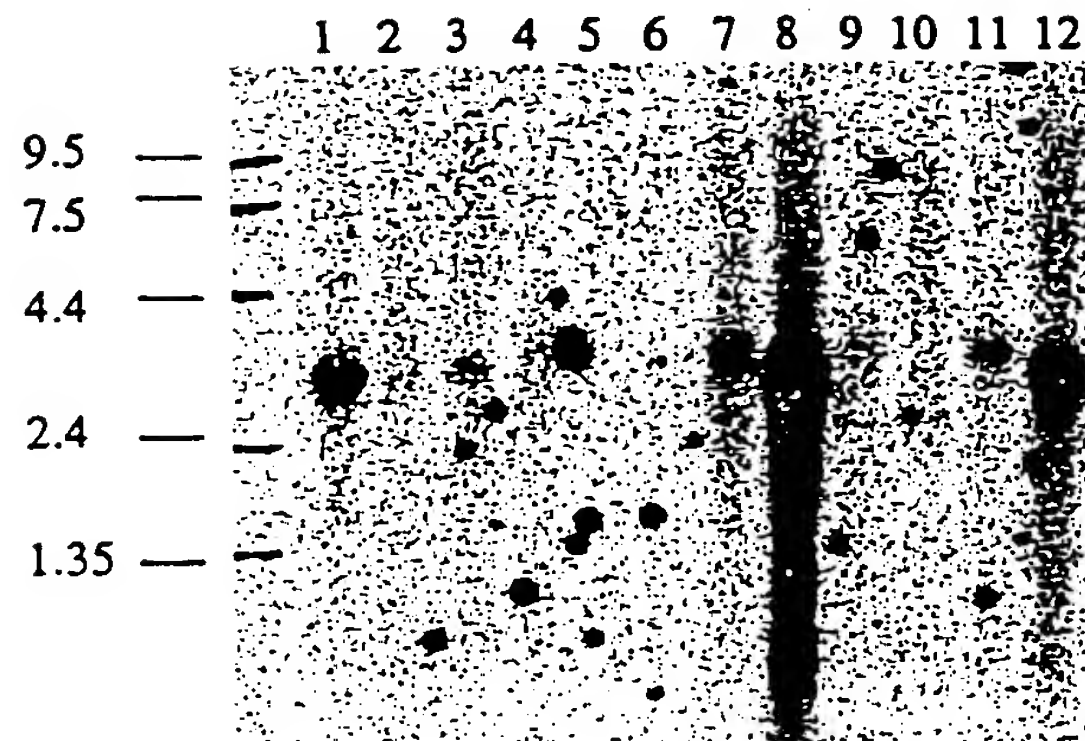


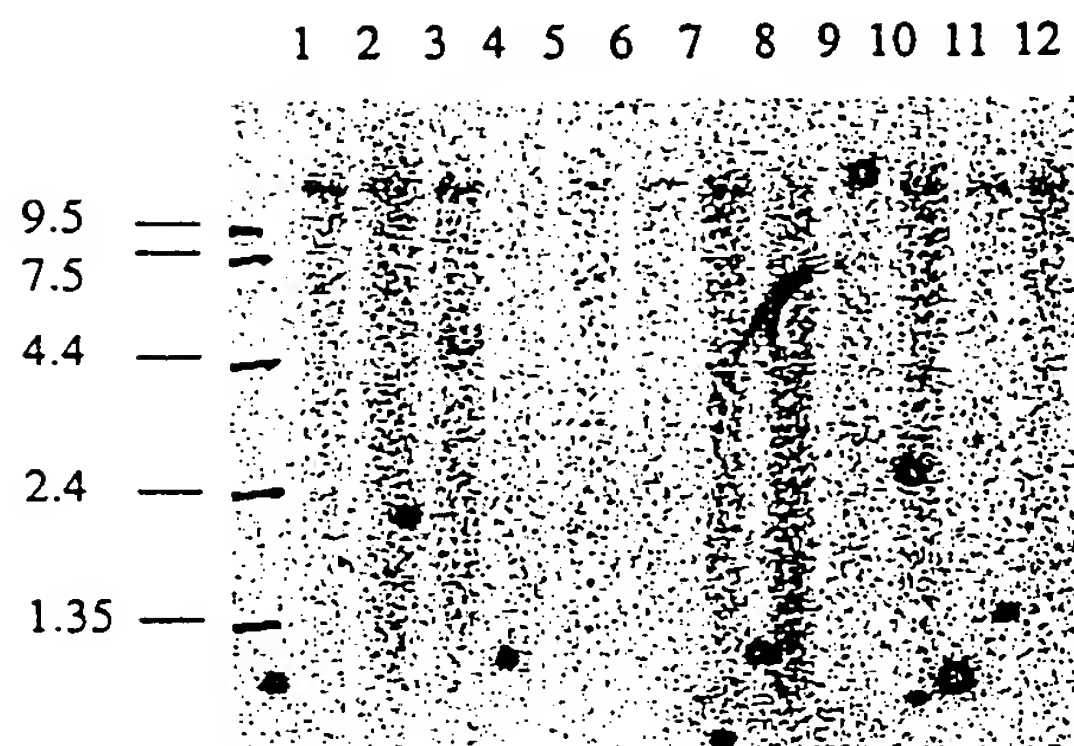
FIG. 6 H

# Gene 583



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

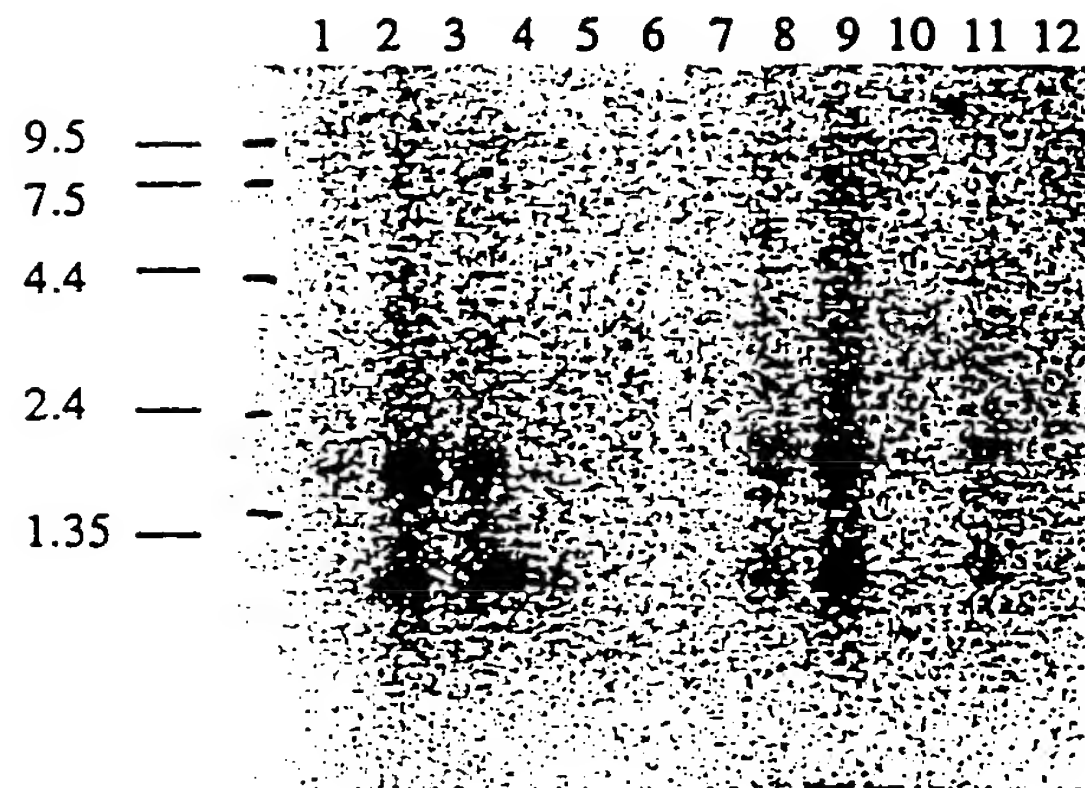
# Gene 589



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

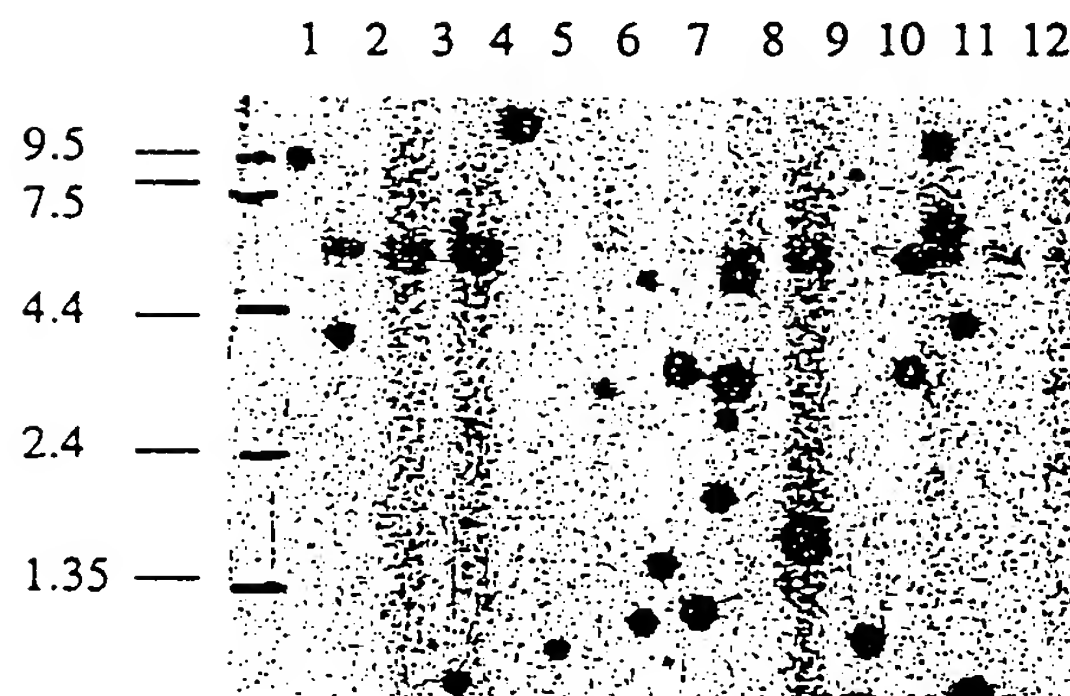
FIG. 6 I

# Gene 590



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

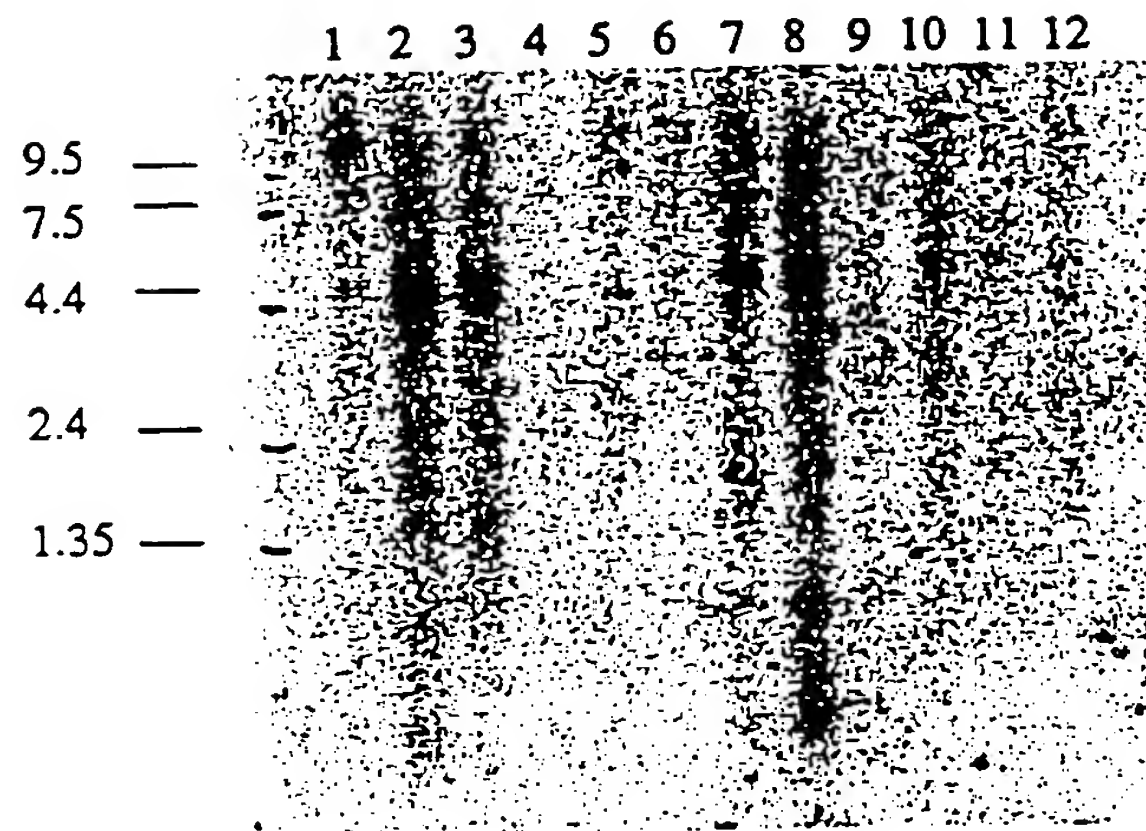
# Gene 592



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

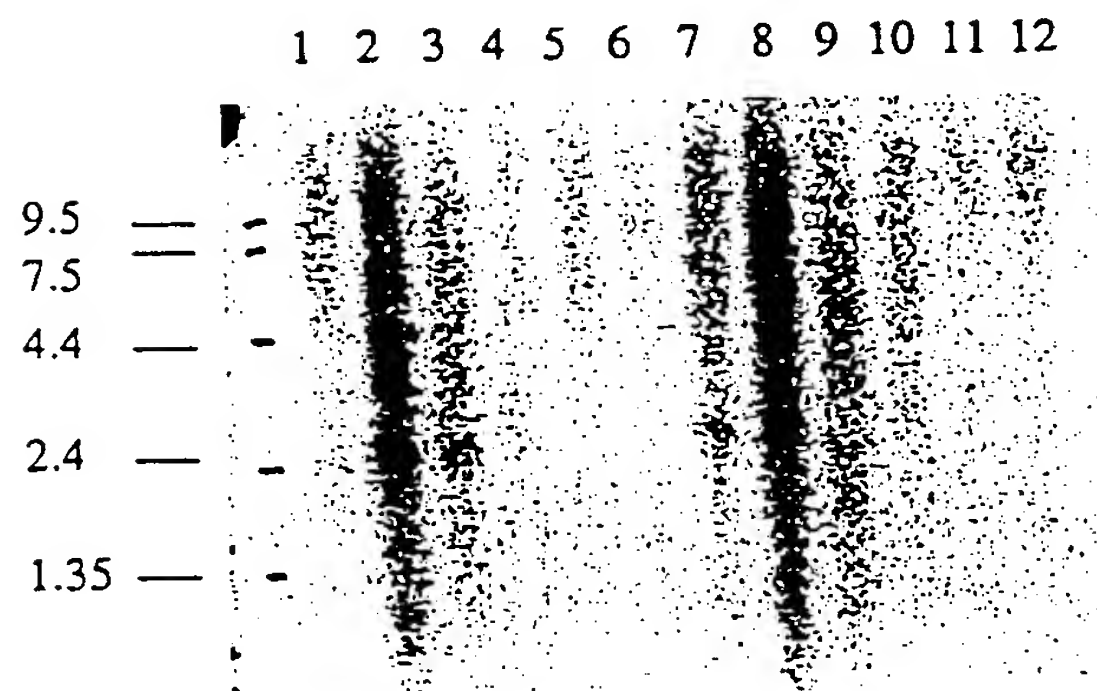
FIG. 6 J

# Gene 594



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

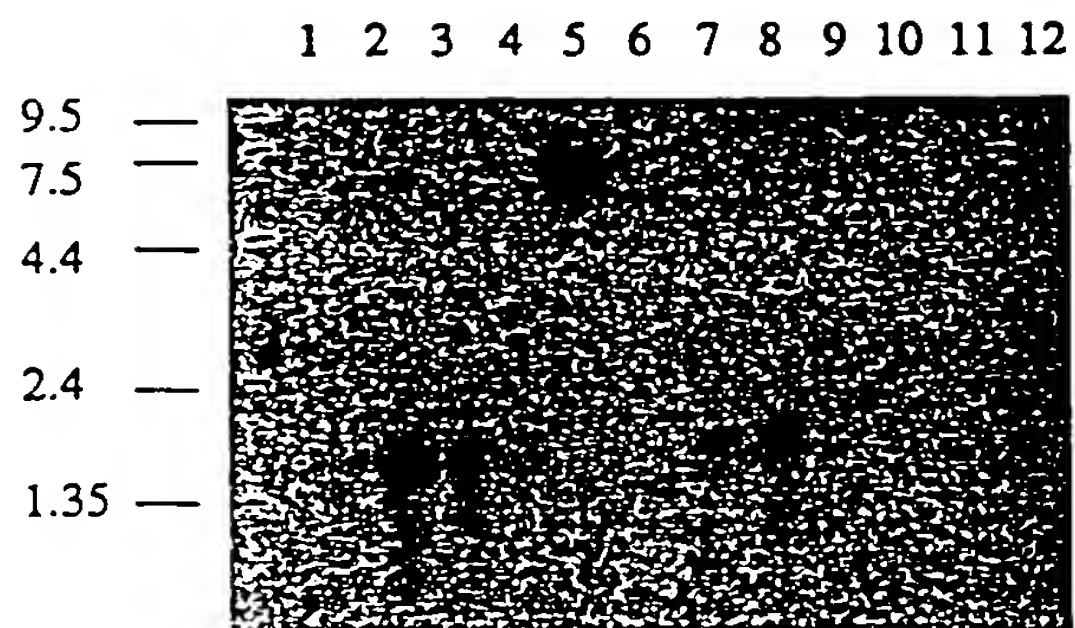
# Gene 595



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

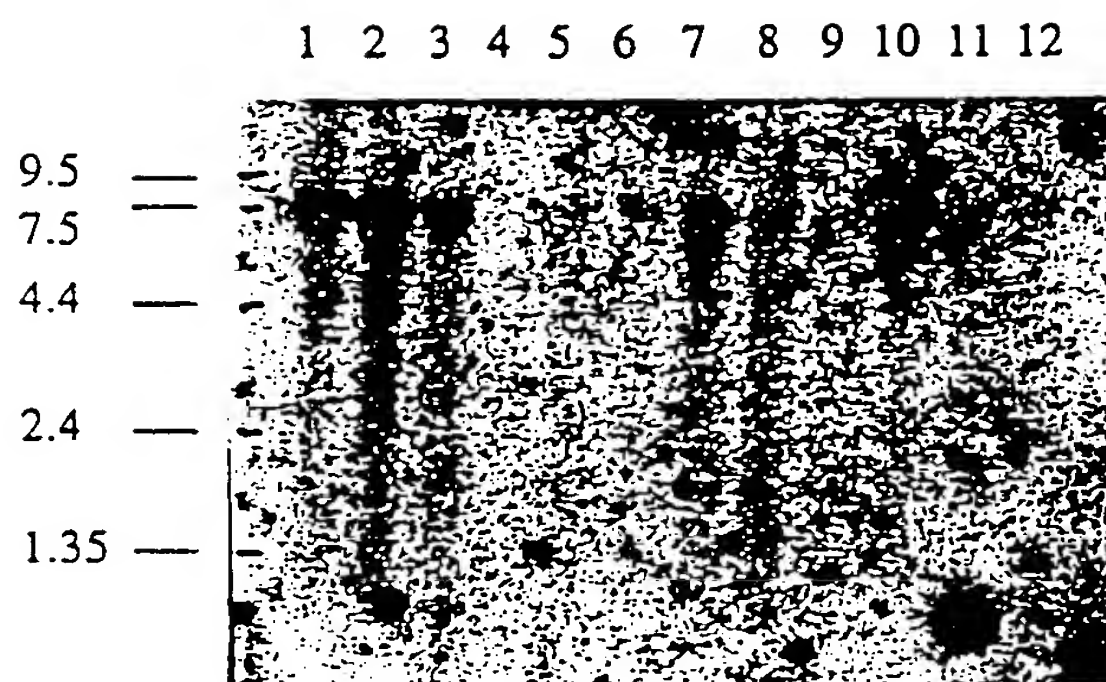
FIG. 6 K

# Gene 596



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

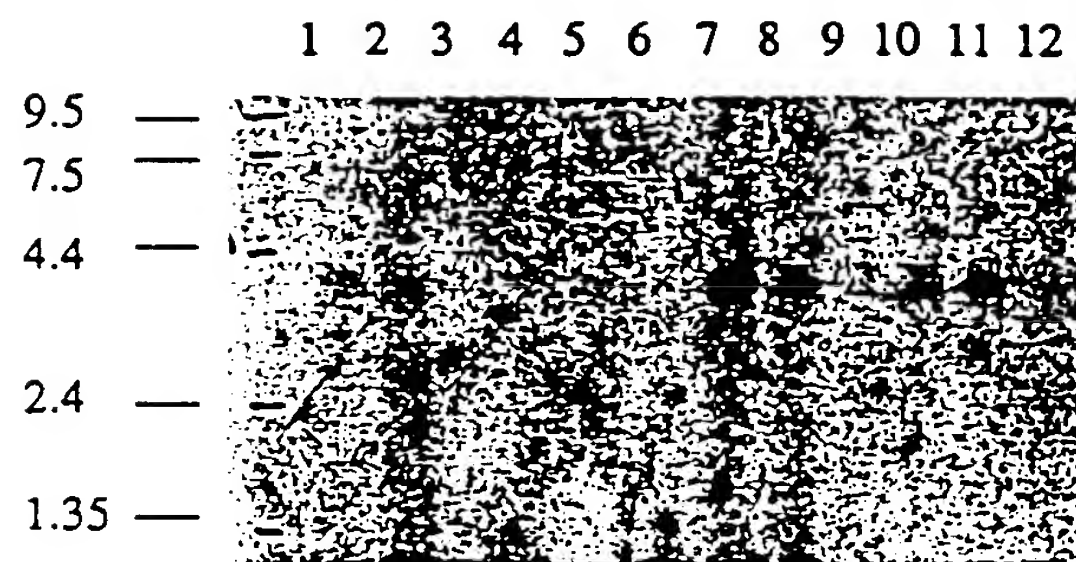
# Gene 604



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

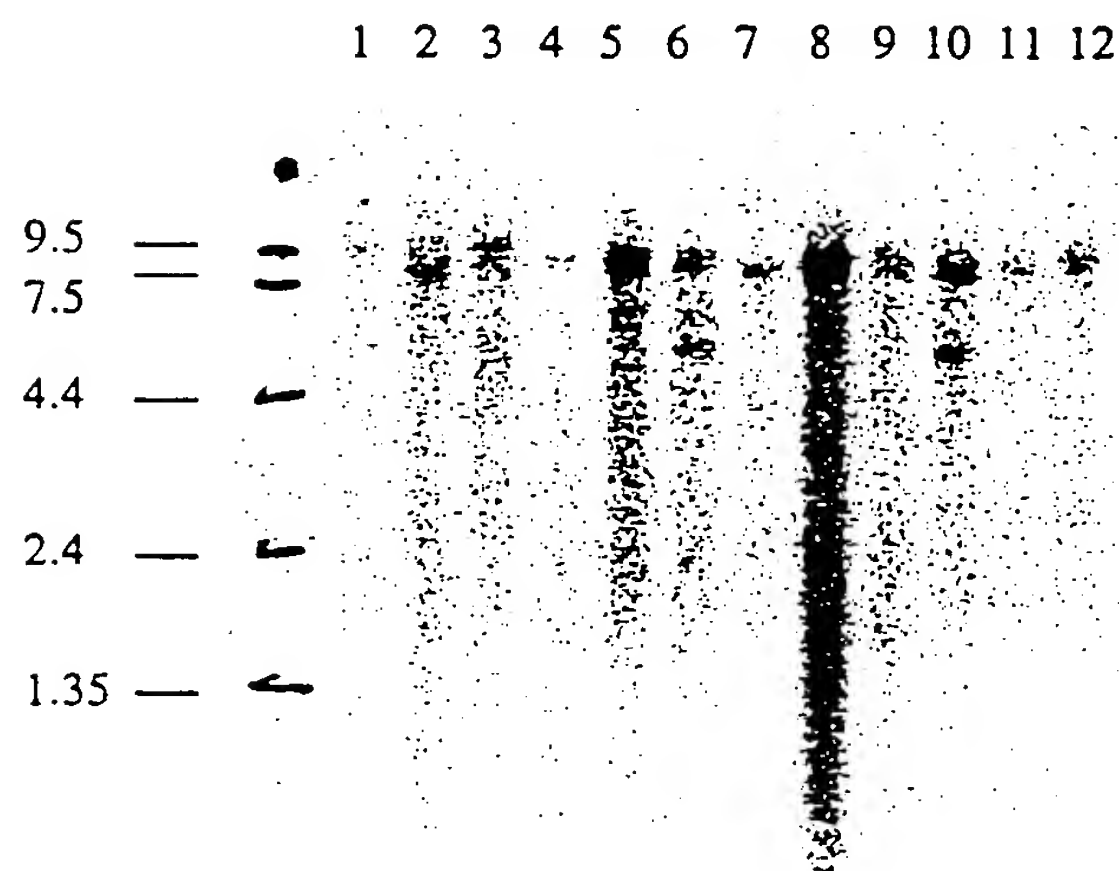
FIG. 6 L

# Gene 605



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

# Gene 606

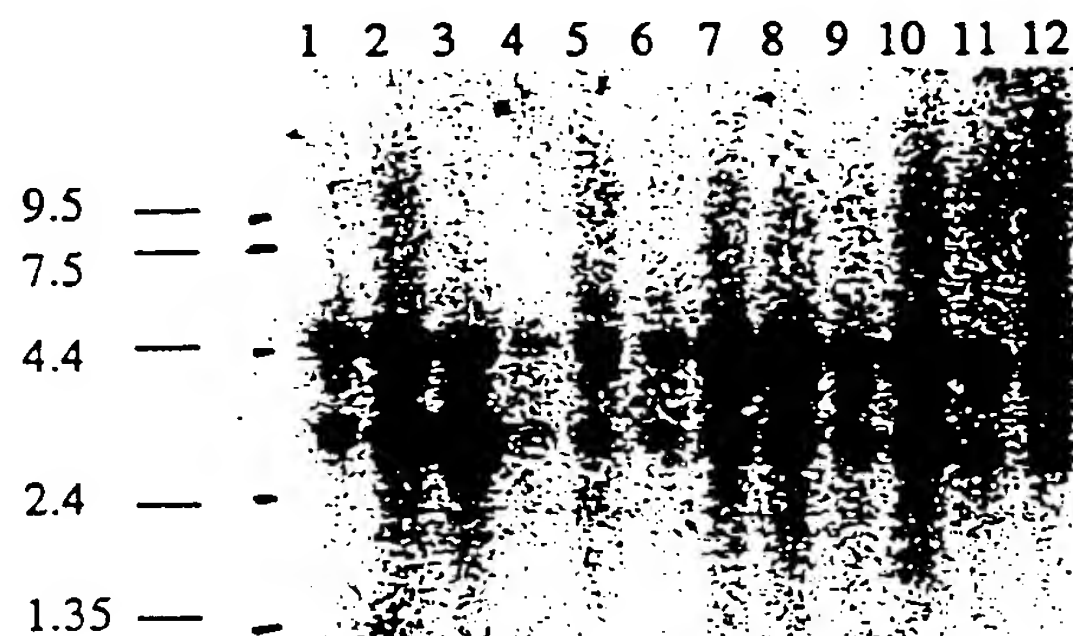


1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 M

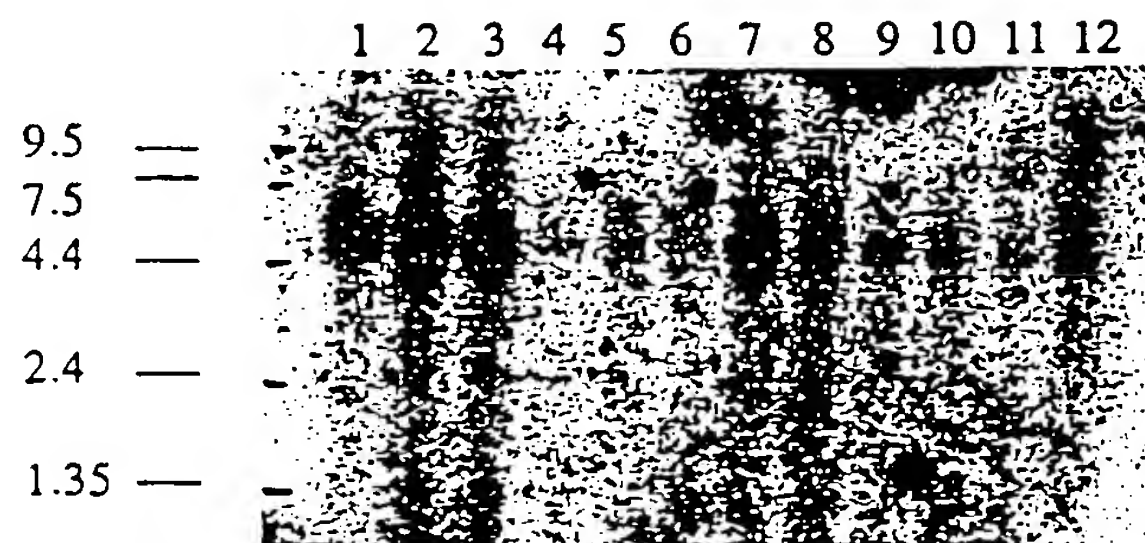


# Gene 608



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

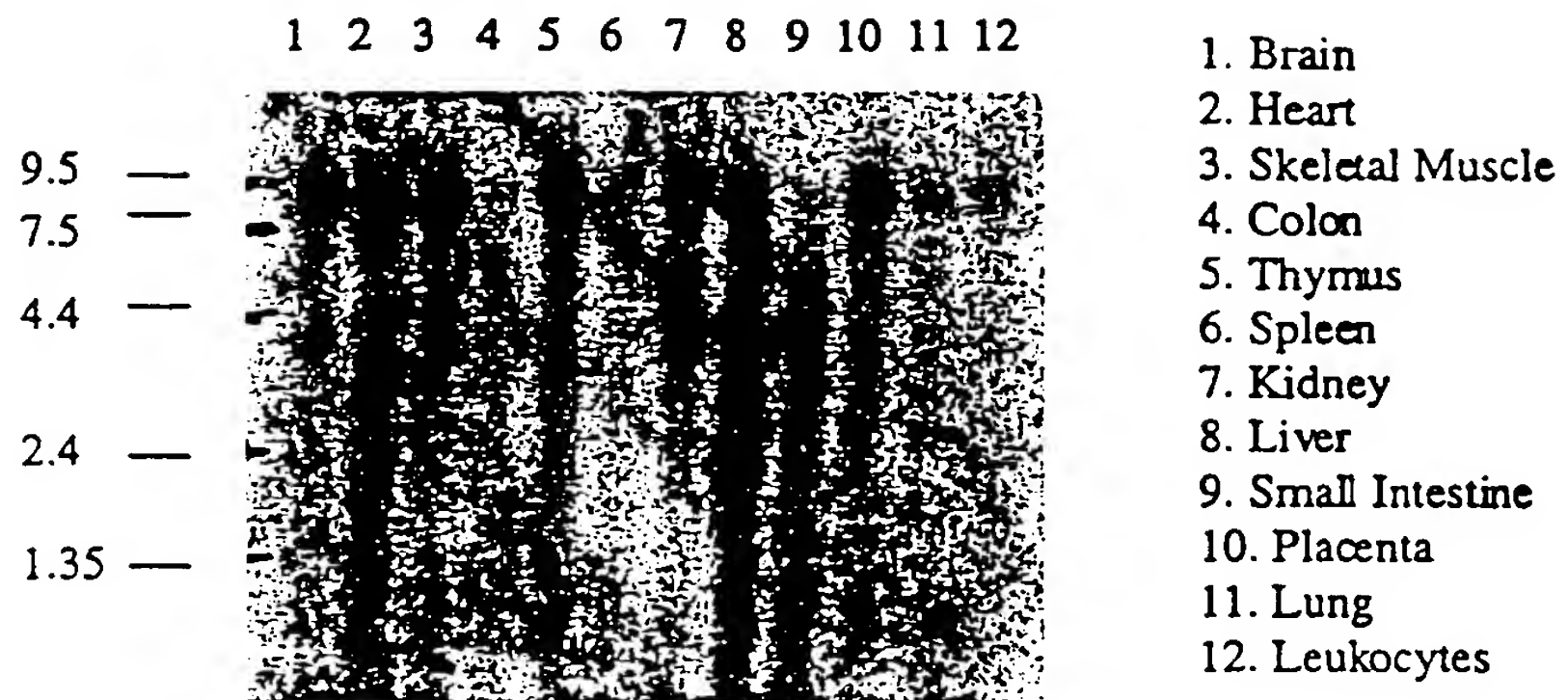
# Gene 611



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 N

# Gene 615



# Gene 617

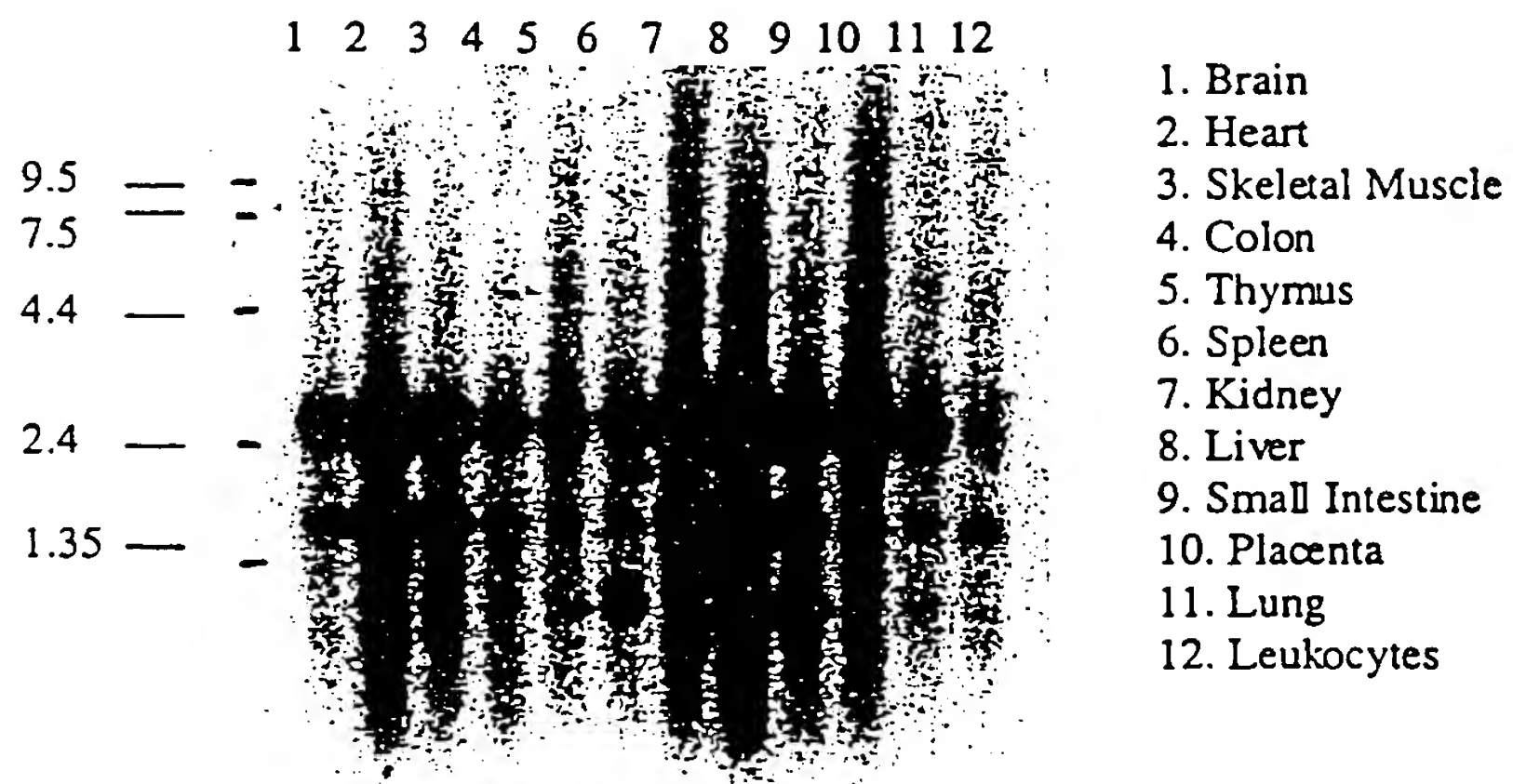
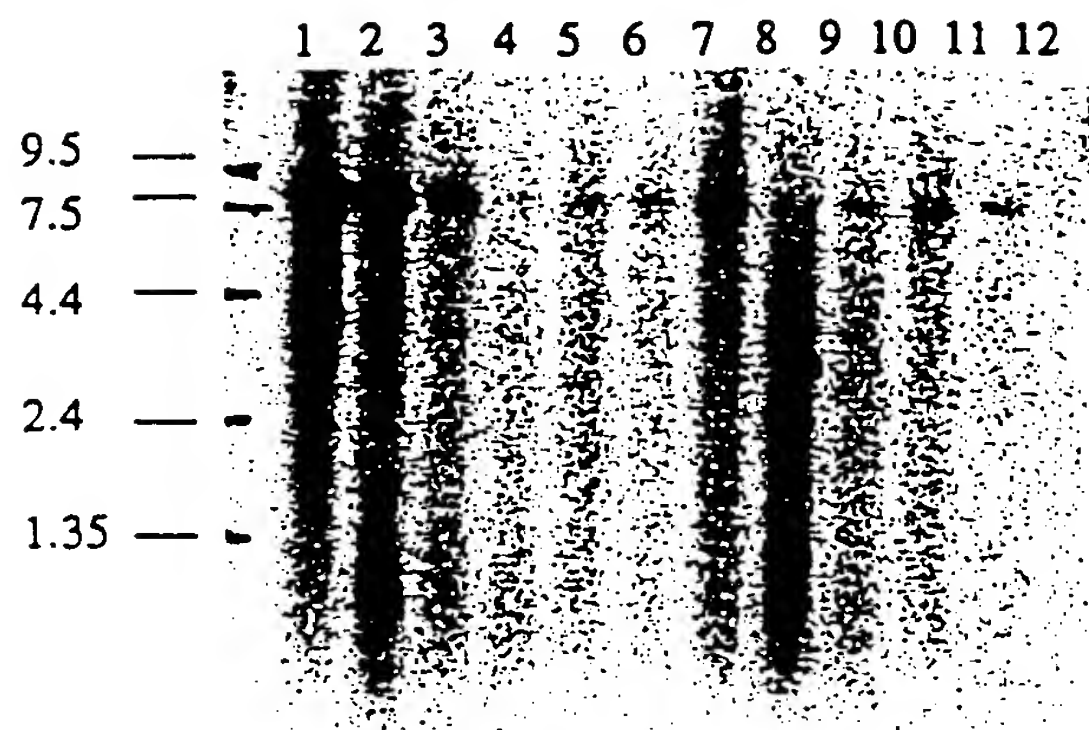


FIG. 6 O

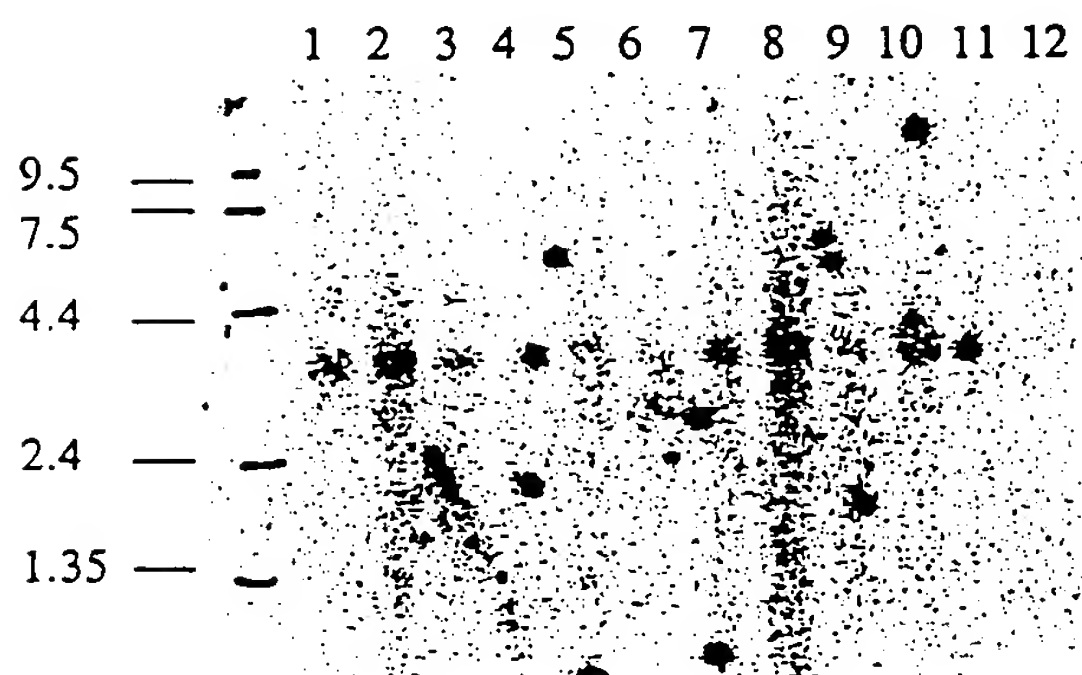


# Gene 618



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

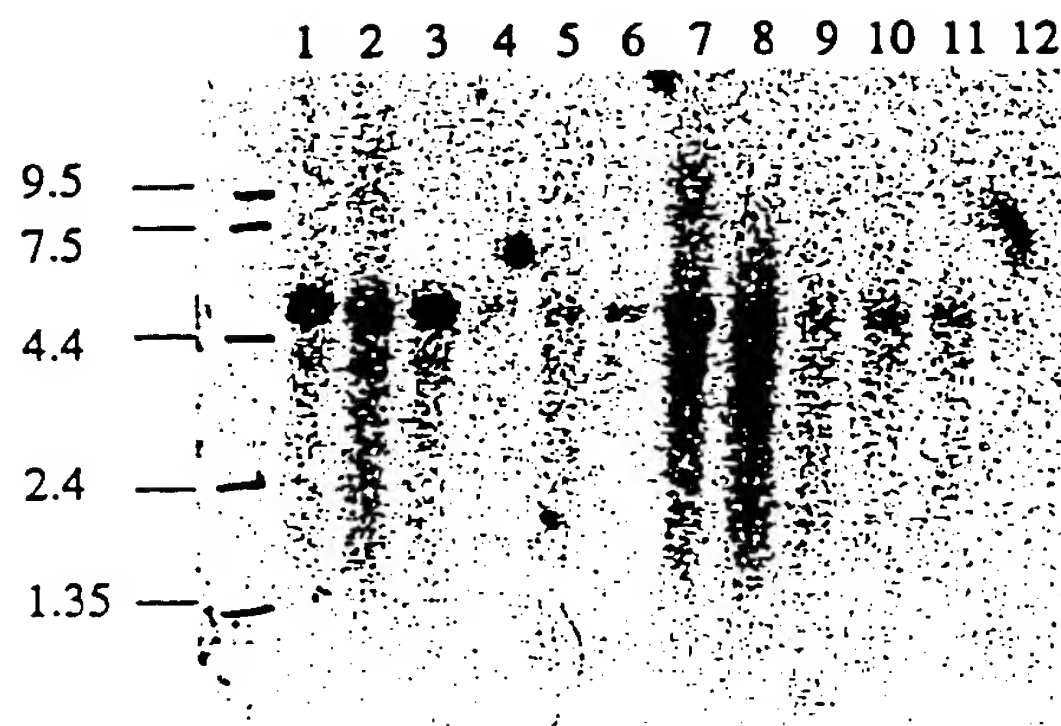
# Gene 619



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

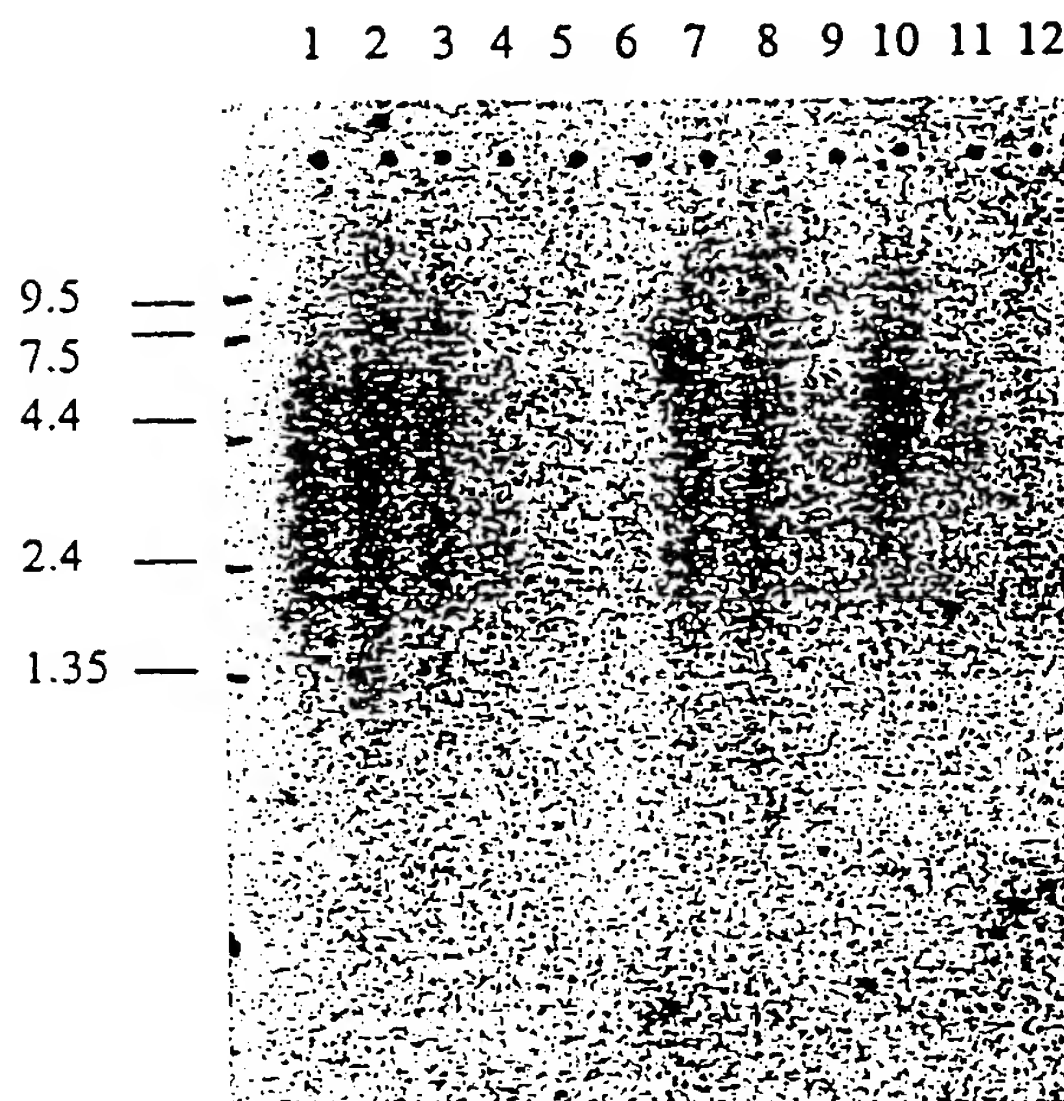
FIG. 6 P

# Gene 621



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

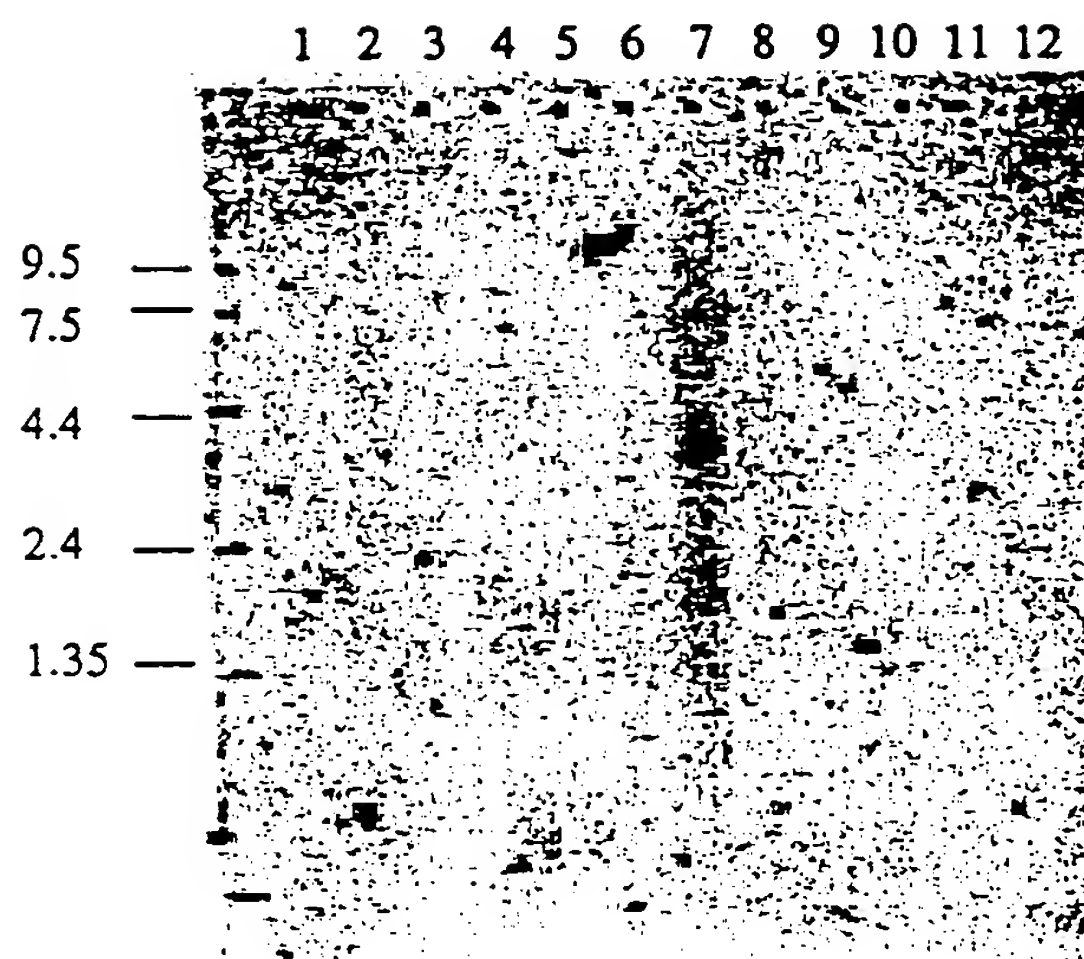
# Gene 693



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

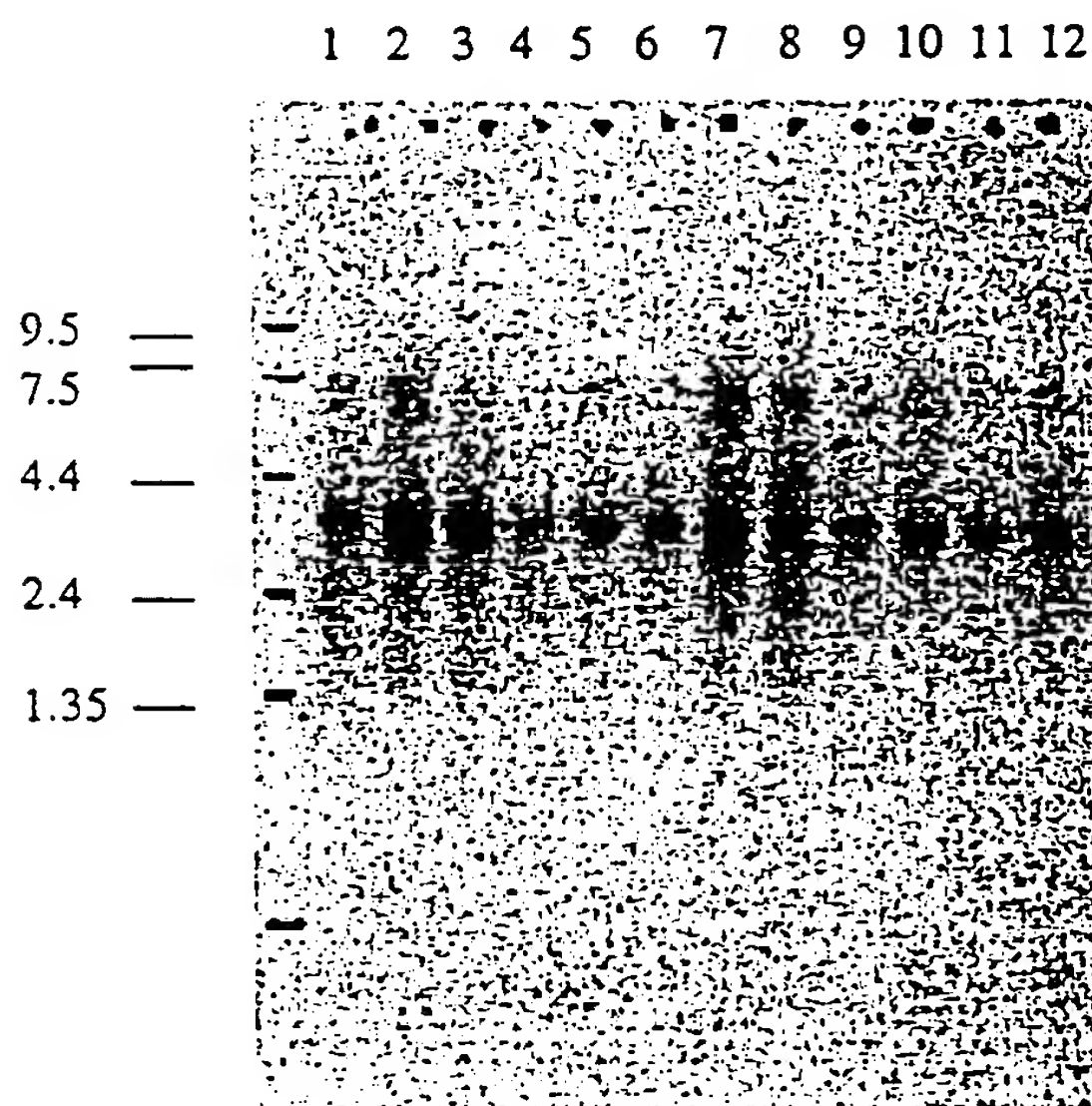
FIG. 6 Q

# Gene 698



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

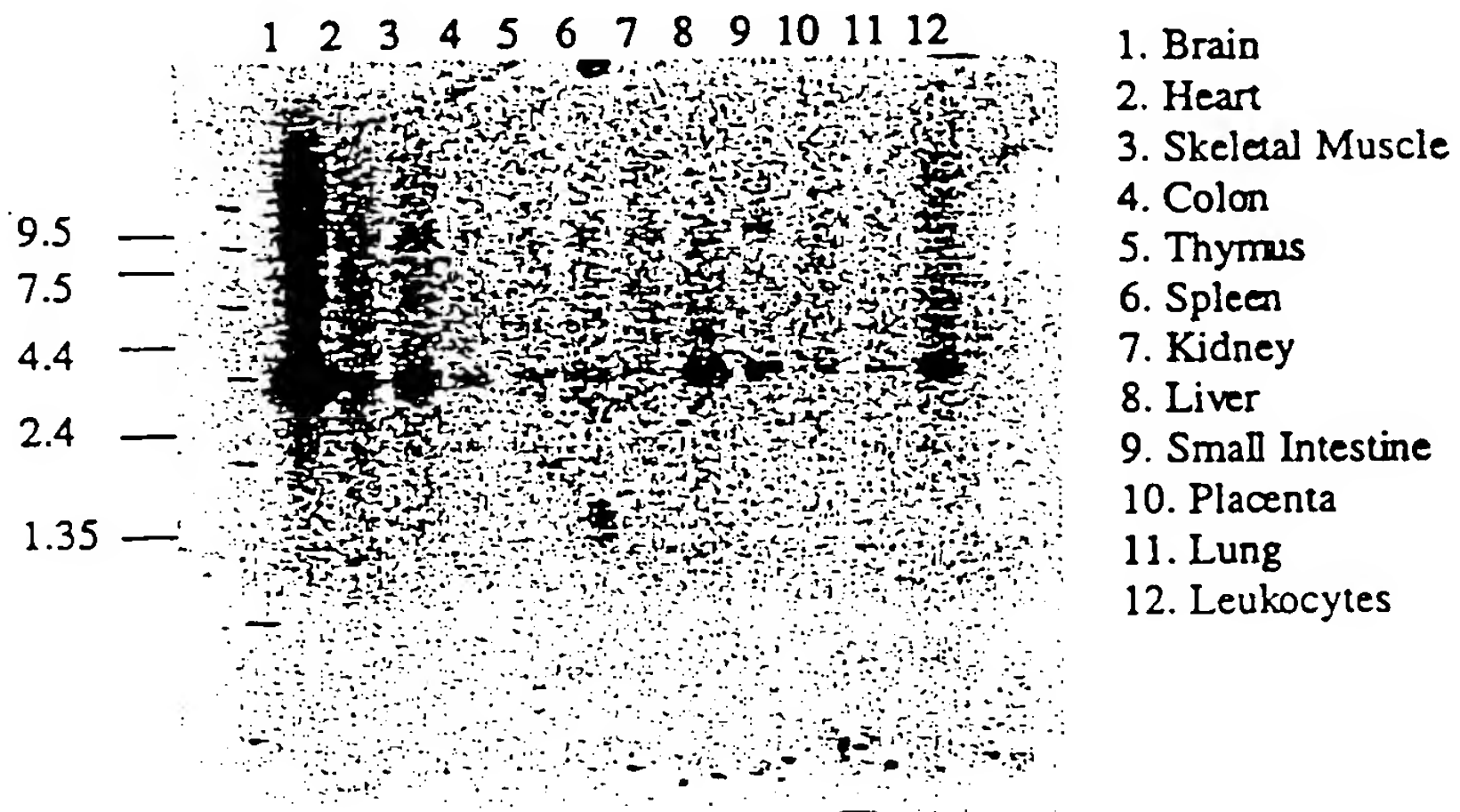
# Gene 699



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 R

# Gene 702



# Gene 722

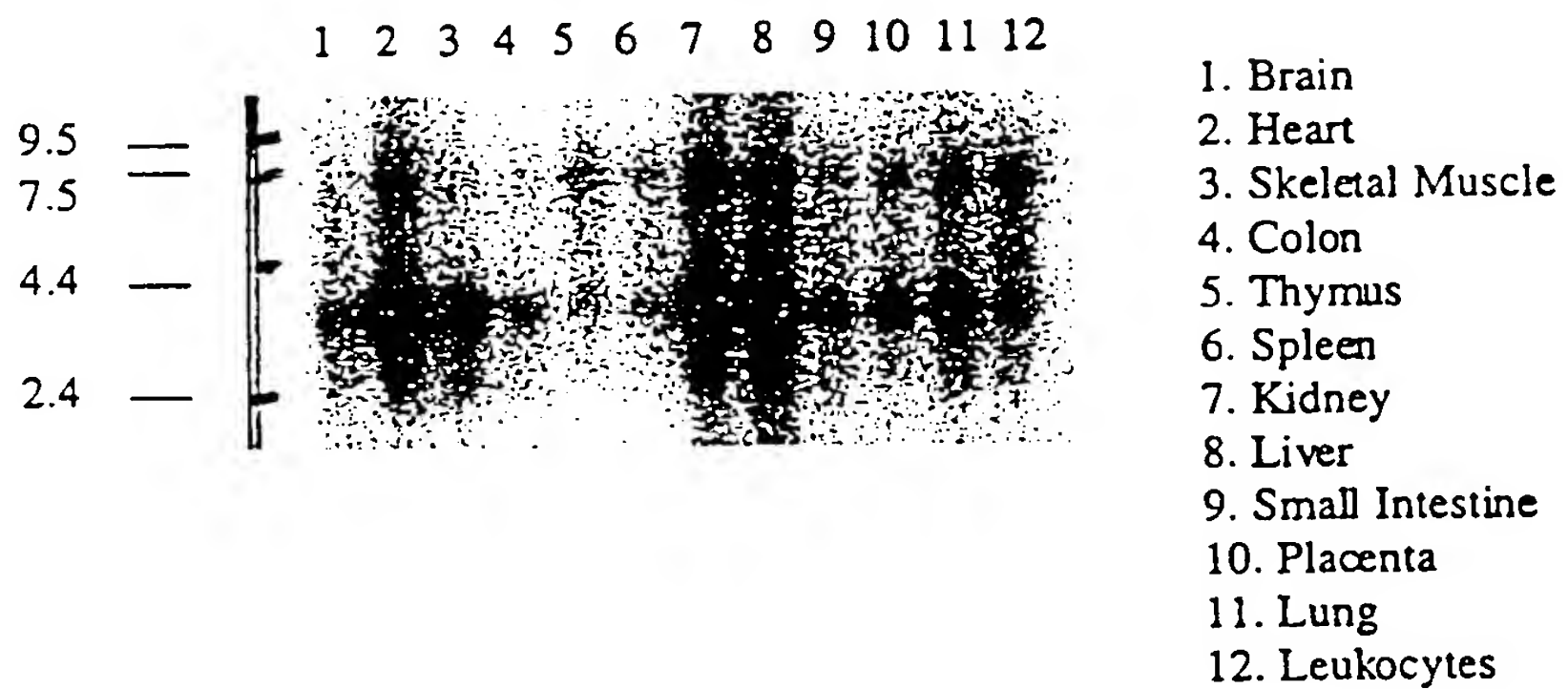
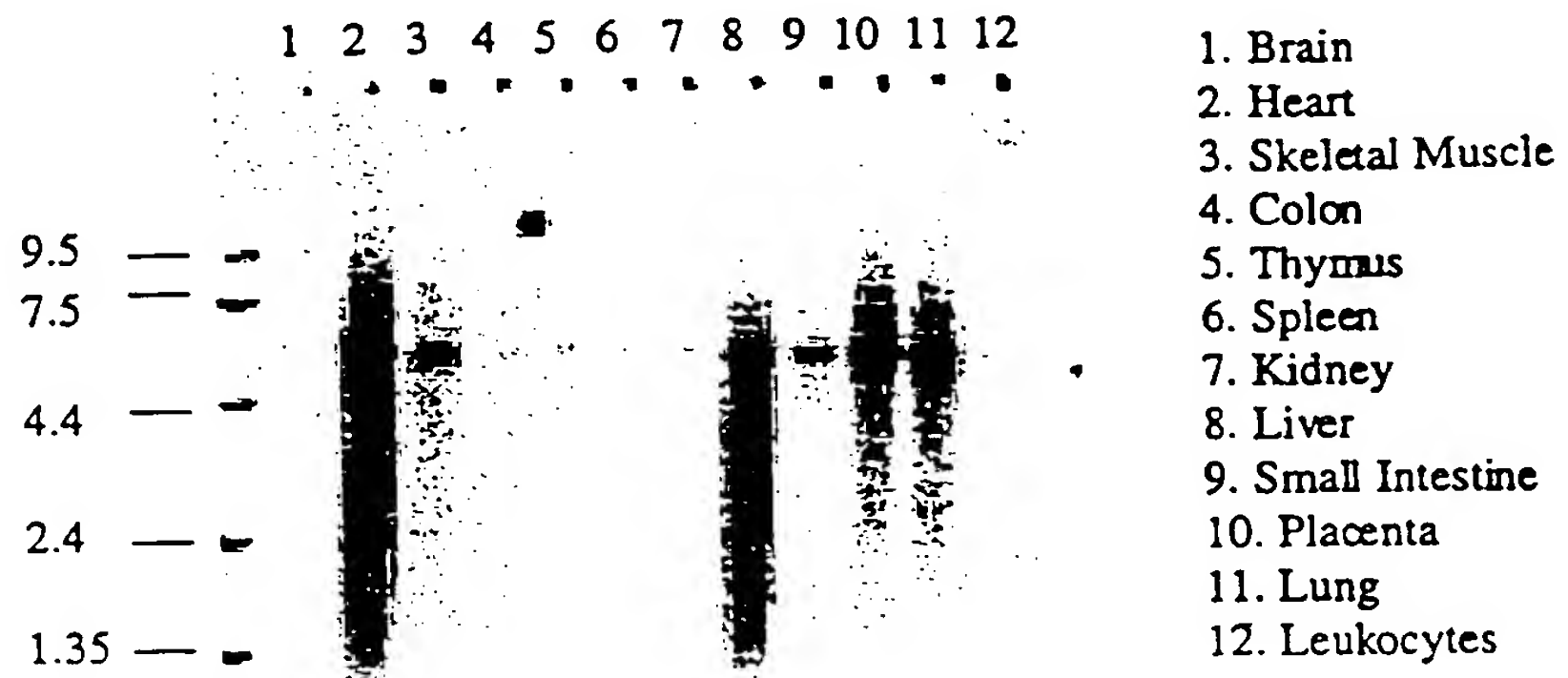


FIG. 6 S

# Gene 751



# Gene 756

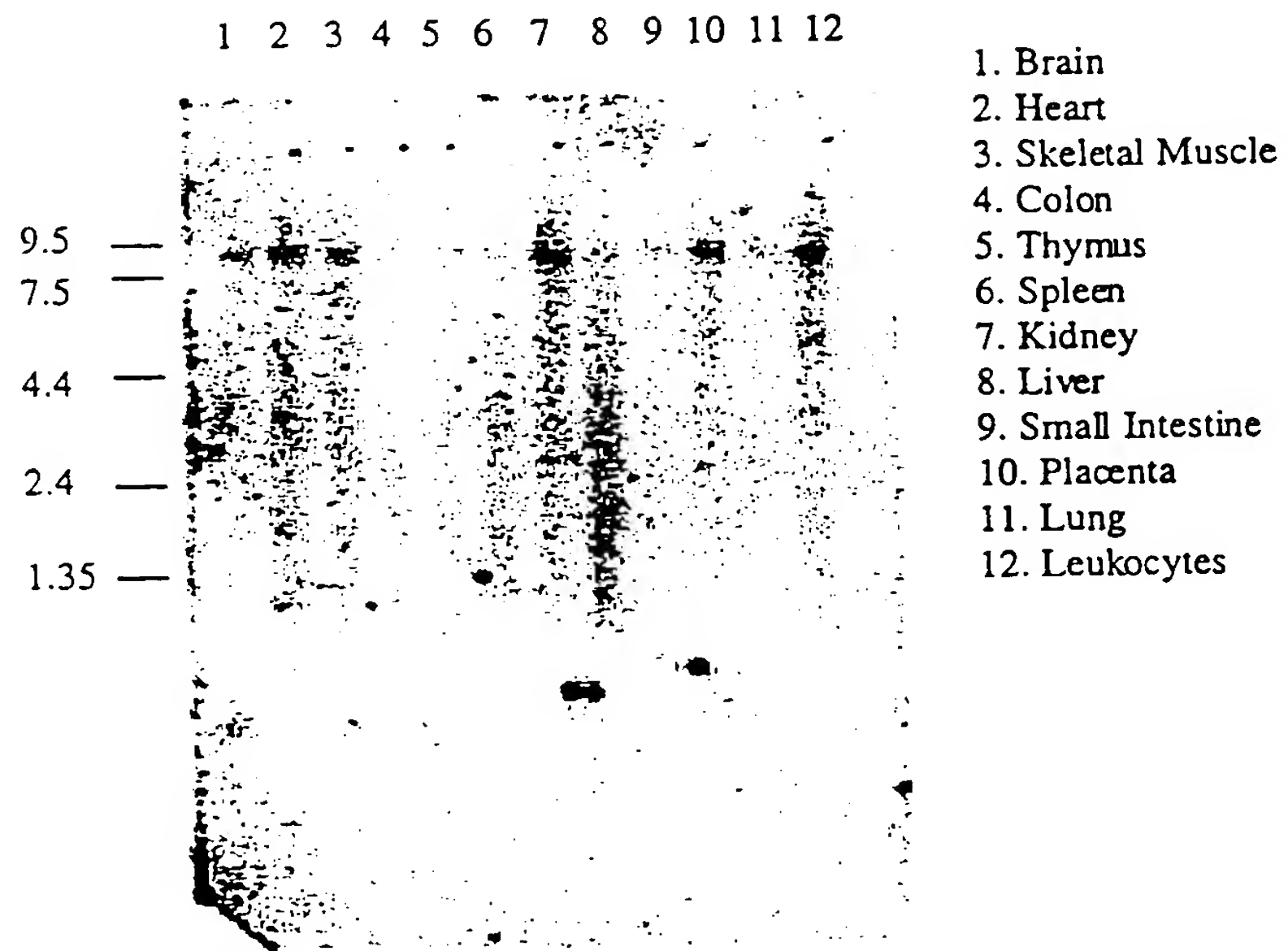
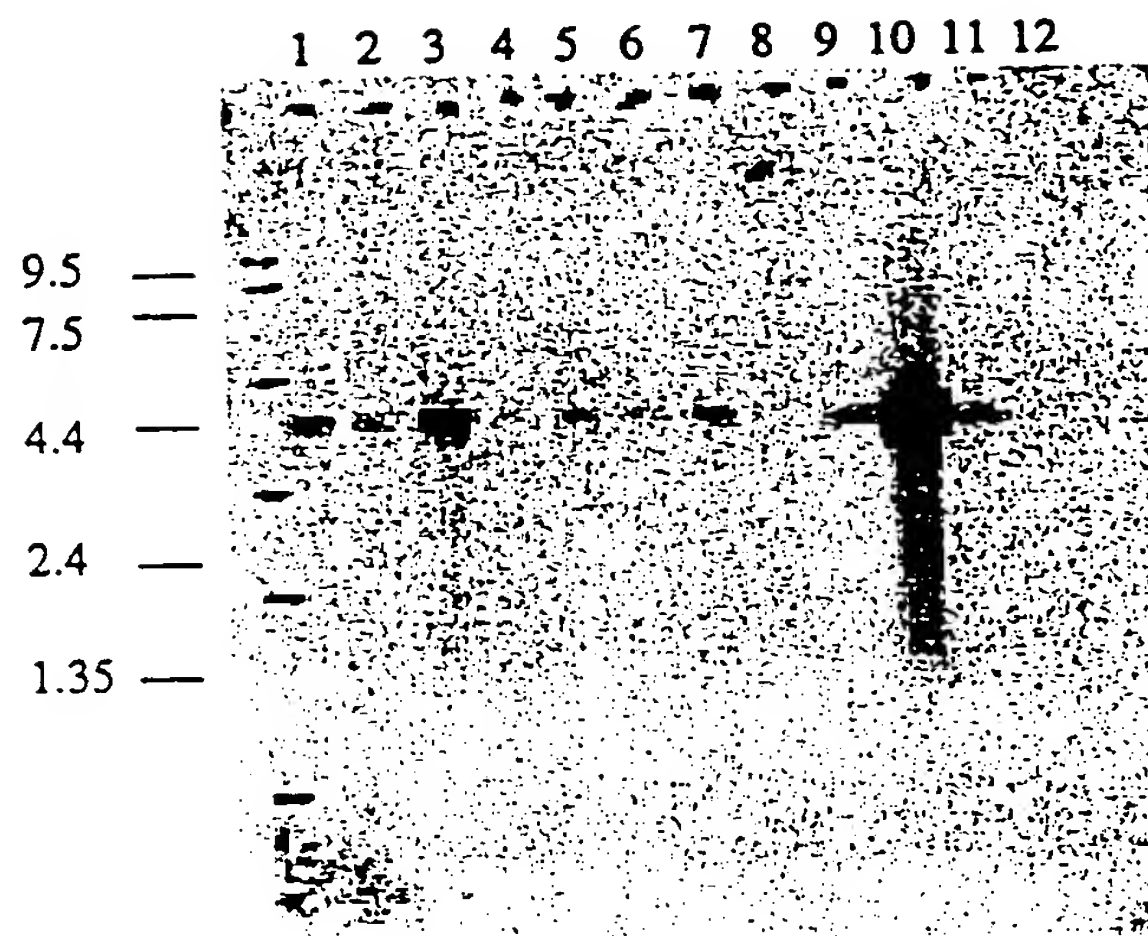


FIG. 6 T

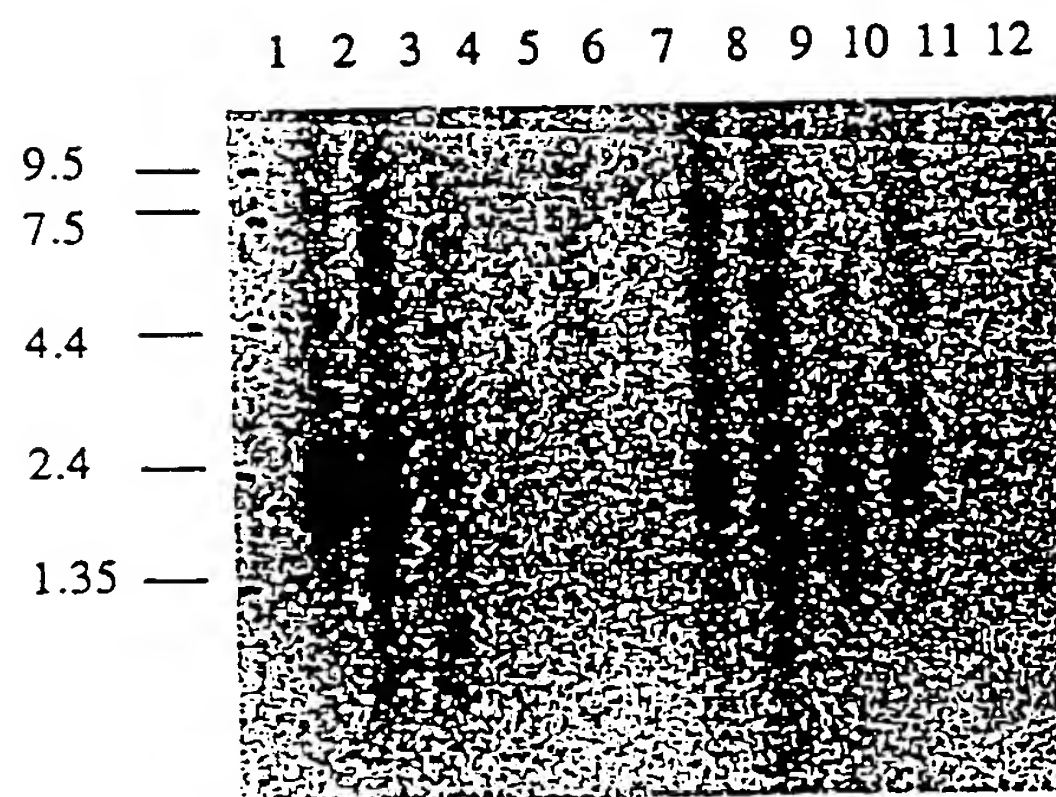


# Gene 757



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

# Gene 848



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 U

10	30	50
GCTTGCTGTGGCCCTGTCAGGAAGAGTAGAGCTCTGGTCCAGCTCCGCGCAGGGAGGGAG		
70	90	110
GCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTTCCAGTATGAGACGAACAAA MetProAlaCysCysSerCysSerAspValPheGlnTyrGluThrAsnLys		
130	150	170
GTCACCTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTTCCACGTGATCATC ValThrArgIleGlnSerMetAsnTyrGlyThrIleLysTrpPhePheHisValIleIle		
190	210	230
TTTTCCTACGTTTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGAGCCTGTC PheSerTyrValCysPheAlaLeuValSerAspLysLeuTyrGlnArgLysGluProVal		
250	270	290
ATCAGTTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGAGGAGATCGTGGAG IleSerSerValHisThrLysValLysGlyIleAlaGluValLysGluGluIle <u>Val</u> Glu		
310	330	350
AATGGAGTGAAGAAGTTGGTGACAGTGTCTTTGACACCGCAGACTACACCTTCCCTTTG AsnGlyValLysLysLeuValHisSerValPheAspThrAlaAspTyrThrPheProLeu		
370	390	410
CAGGGGAACCTCTTTCTTCGTGATGACAACTTTCTCAAAACAGAAGGCCAAGAGCAGCGG GlnGlyAsnSerPhePheValMetThrAsnPheLeuLysThrGluGlyGlnGluGlnArg		
430	450	470
TTGTGTCCCGAGTATCCCACCCGCAGGACGCTCTGTTCTCTGACCGAGGTTGTAAAAAG LeuCysProGluTyrProThrArgArgThrLeuCysSerSerAspArgGlyCysLysLys		
490	510	530
GGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCGGAAGGTGTGTAGTGCATGAAGGG GlyTrpMetAspProGlnSerLysGlyIleGlnThr <u>Gly</u> ArgCysValVal <u>His</u> GluGly		
550	570	590

FIG. 7 A

AACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGGAAGAGGCCCCC  
AsnGlnLysThrCysGluValSerAlaTrpCysProIleGluAlaValGluGluAlaPro

610 630 650  
CGGCCTGCTCTCTTGAACAGTGCCGAAACTTCACTGTGCTCATCAAGAACAATATCGAC  
ArgProAlaLeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAsp

670 690 710  
TTCCCCGGCCACAACACTACACCACGAGAAACATCCTGCCAGGTTTAAACATCACTTGTACC  
PheProGlyHisAsnTyrThrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThr

730 750 770  
TTCCACAAGACTCAGAATCCACAGTGTCCCATTTTCCGACTAGGAGACATCTTCCGAGAA  
PheHisLysThrGlnAsnProGlnCysProIlePheArgLeuGlyAspIlePheArgGlu

790 810 830  
ACAGGCGATAATTTTTCAGATGTGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTAC  
ThrGlyAspAsnPheSerAspValAlaIleGlnGlyGlyIleMetGlyIleGluIleTyr

850 870 890  
TGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCGTCCCCAAATACAGTTTCCGTCGC  
TrpAspCysAsnLeuAspArgTrpPheHisHisCysArgProLysTyrSerPheArgArg

910 930 950  
CTTGACGACAAGACCACCAACGTGTCCTTGTACCCTGGCTACAACCTCAGATACGCCAAG  
LeuAspAspLysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLys

970 990 1010  
TACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTTCGGGATCCGTTTT  
TyrTyrLysGluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPhe

1030 1050 1070  
GACATCCTGGTTTTTGGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATC  
AspIleLeuValPheGlyThrGlyGlyLysPheAspIleIleGlnLeuValValTyrIle

1090 1110 1130  
GGCTCAACCTCTCCTACTTCGGTCTGGCCACTGTGTTTCATCGACTTCCTCATCGACACT  
GlySerThrLeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThr

FIG. 7 B



1150	1170	1190
TACTCCAGTAACTGCTGTCGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCAGCCCTGT		
TyrSerSerAsnCysCysArgSerHisIleTyrProTrpCysLysCysCysGlnProCys		
1210	1230	1250
GTGGTCAACGAATACTACTACAGGAAGAAGTGCGAGTCCATTGTGGAGCCAAAGCCGACA		
ValValAsnGluTyrTyrTyrArgLysLysCysGluSerIleValGluProLysProThr		
1270	1290	1310
TTAAAGTATGTGTCCTTTGTGGATGAATCCCACATTAGGATGGTGAACCAGCAGCTACTA		
LeuLysTyrValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeu		
1330	1350	1370
GGGAGAAGTTTGCAAGATGTCAAGGGCCCAAGAAGTCCCAAGACCTGCGATGGACTTCACA		
GlyArgSerLeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThr		
1390	1410	1430
GATTGTCCAGGCTGCCCCTGGCCCTCCATGACACACCCCGATTCTGACCAACCAGAG		
AspLeuSerArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGlu		
1450	1470	1490
GAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAGCCCCGTCTGGTGC		
GluIle <u>Gln</u> LeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTrpCys		
1510	1530	1550
CAGTGTGGAAGATGCCTCCCATCTCAACTCCCTGAGAGCCACAGGTGCCTGGAGGAGCTG		
GlnCysGlyArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGlu <u>Glu</u> Leu		
1570	1590	1610
TGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACTCAGAGCTGTTTCAGGAAGCTGGTC		
CysCysArgLysLysProGlyAlaCysIleThrThrSerGluLeuPheArgLysLeuVal		
1630	1650	1670
CTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGCCCTTGCTGGCGCTGGAT		
LeuSerArgHisValLeuGlnPheLeuLeuLeuTyrGlnGluProLeuLeuAlaLeuAsp		
1690	1710	1730

FIG. 7 C

GTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCCTACAGGTGCTACGCCACCTGGCGC  
ValAspSerThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTrpArg

1750 1770 1790  
TTCGGCTCCCAGGACATGGCTGACTTTGCCATCCTGCCCAGCTGCTGCCGCTGGAGGATC  
PheGlySerGlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTrpArgIle

1810 1830 1850  
CGGAAAGAGTTTCCAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAGTCCTTACTGAAGC  
ArgLysGluPheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyrEnd

1870 1890 1910  
CAGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTTTGGGAGGCCGAGGCAGGCAGATCA

1930 1950 1970  
CCTGAGATCGGGAGTTGGAGACCCGCCTGGCTAACAAGGCGAAATCCTGTCTGTACTAAA

1990 2010 2030  
AATACAAAATCAGCCAGACATGGTGGCATGCACCTGCAATCCCAGCTACTCGGGAGGCT

2050 2070 2090  
GAGGCACAAGAATCACTTGAACCCGGGAGGCAGAGGTTGTAGTGAGCCCAGATTGTGCCA

2110 2130 2150  
CTGCTCTCCAGCCTGGGAGGCACAGCAAACCTGTCCCCAAAAAAAAAAAAAGAGTCCTTAC

2170 2190 2210  
CAATAGCAGGGGCTGCAGTAGCCATGTTAAACATGACATTTACCAGCAACTTGAAC TTCAC

2230 2250 2270  
CTGCAAAGCTCTGTGGCCACATTTTCAGCCAAAGGGAAATATGCTTTCATCTTCTGTTGC

2290 2310 2330  
TCTCTGTGTCTGAGAGCAAAGTGACCTGGTTAAACAAACCAGAATCCCTCTACATGGACT

2350 2370 2390

FIG. 7 D

CAGAGAAAAGAGATTGAGATGTAAGTCTCAACTCTGTCCCCAGGAAGTTGTGTGACCCTA

2410

2430

2450

GGCCTCTCACCTCTGTGCCTCTGTCTCCTTGTTGCCCACTACTATCTCAGAGATATTGT

2470

2490

2510

GAGGACAAATTGAGACAGTGCACATGAACTGTCTTTTAATGTGTAAAGATCTACATGAAT

2530

2550

2570

GCAAAACATTTTCATTATGAGGTCAGACTAGGATAATGTCCAACTAAAAACAAACCCTTTT

2590

2610

2630

CATCCTGGCTGGAGAATGTGGAGAACTAAAGGTGGCCACAAATTCTTTGACACTCAAGTC

2650

2670

2690

CCCCAAGACCTAAGGGTTTTATCTCCTCCCCTTGAATATGGGTGGCTCTGATTGCTTTAT

2710

2730

2750

CCAAAAGTGGAAGTGACATTGTGTCAGTTTCAGATCCTGATCTTAAGAGGCTGACAGCTT

2770

2790

2810

CTACTTGCTGTCCCTTGGAACCTCTTGCTATCGGGGAAGCCAGACGCCATTTAAAAGTCTG

2830

2850

2870

CCTATCCTGGCCAGGTGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGACCAAGG

2890

2910

2930

CGGGCGGATCACTTAAAGTCAGGAGTCCAAGACCAGACTCGCCAACATGGTGAAACCGTA

2950

2970

2990

TCTCTAATAAAAATACAAAAATTAGCTGGGCATGGTGCGGGCACCTGTAGTCCTAGCTAT

3010

3030

3050

CAAGAGGCTGAGACAGGAGAAACACTTGAACCTGGGAGGTGGAGGTTGCATTGAGCTGAG

FIG. 7 E

3070	3090	3110
ATCGTGCCACTGCACTCCAGGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAAAAAA		
3130	3150	3170
AAAAGAAAAAAAAAATGTCTGCCTATCCTGAGACTGCCCTGCTGTGAGGAAGCCCAAGCA		
3190	3210	3230
GTCACGTGGACAGTGCCTGACCAGCCCCAGCTTTCAAGCCATCCAAGCCCAGTCACCAA		
3250	3270	3290
CATGAGAGAGAAGAAGCCTTCAGGTGATTCTGGACTCCACTAACATATGACTGATACCGC		
3310	3330	3350
ATGATACATCCCAAGTGAGAACTGCCCCATAAATCCAGAAAACCACATTGCTATCTTAAG		
3370	3390	3410
TCCCTAAGTTTGGGGCTTATTTGTTCCACAGCAACAGGTAAGTGGAACAGAGGGCAAGCC		
3430	3450	3470
TGATGAATGGGCACACAGACTCAGCCCATACCTTCCCTGGTTCTAATGTTCTCAGGGAGC		
3490	3510	3530
CCGGACCAACCCTGGGAGCCTCAGGAACTTAGGTTTCCACTGGACAGTTCTAGAAGGGCT		
3550	3570	3590
ATAGACCAAATCAGGTAACCTACCAGACCAGCCTTGGAATCTATCAAATCTAACTGCTGA		
3610	3630	3650
GCTACCCAGTGCATTCCGATCCTCATCACAATTCTTTGACTGAAGGCCGGGCGTGGTGGC		
3670	3690	3710
TCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACCTGAGGTCAGGA		

FIG. 7 F

3730	3750	3770
GTTGAGACCAGCCTGGCCAACATGGTGAGACCCTGTCTCTACTAAGAATACAAAATTA		
3790	3810	3830
GGTGGGGTGGCGGTGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATC		
3850	3870	3890
TCTTGAACCTGGAAGGTGGAGGTTGCAATAAGCCGAGATAGTGCCACTGCACTCCAGCCT		
3910	3930	3950
AGATAACAGAGCAAGACTCTGTCTCAAAAAACAACAACAACAACAACAATTTCTAT		
3970	3990	4010
GACTGAAAGTGACTAAAAAGCTGGCTTTATGCCATTAACACTCTGTACTTTGCAGCCAAT		
4030	4050	4070
CAGAACTGACGCAGTCTGGGTGCTAGCTGCTTCAAAGCAACCCACACCACACTTTTACC		
4090	4110	4130
ATTTCCATACATCAACTGCTGAGAATATGAAAATGCACAGTGACAGGTTTTAGGATCCTG		
4150	4170	4190
CTTCAGGATTTTCCTTTTCCTGGTTTGGTCACTAGAGTTGGCTATTTATCTGTTTCTAAAC		
4210	4230	4250
AATAGCTATTTTATCGAATAGTTTAGAGACCACTATTAAATATTGTGACTGATGAAGGAT		
4270	4290	4310
CTGTGAATTTTTTTATATATGTTCTAAGAGTTACCATTTTGATACCTTTTAAAAACCAGC		
4330	4350	4370
AGCTTTCTACTATATTCATGTAAAACAGCATGAATAAAACCATTTTTTGATACAGGGTTT		
4390	4410	4430

FIG. 7 G

TATTTGGCTTTAAACTCAGGAACCAAGTTAATTATGCCAGATTGAACTTTGATTTTACT

4450

4470

4490

ACCTTTTCAAAGATATTTTAAAAAGTGGATTACTACATATGATTTCTTTGGAGCTTACAT

4510

4530

4550

TTCTTTACTTCACGAATTCTATGTCAGTGTACAAGTTTCCATTCTGATGGCTTCTGGGC

4570

4590

4610

CTTTGTACCTTTGTTTTTGGTGCCTTATTCCTAGTATGTTTCTATCACCTTAATGAGGCC

4630

4650

4670

GCAGATGGAGTCAGAATGTGAAATTACAAATAATCACTGGATCCATCTACTGTTTTCCAT

4690

4710

4730

CACCTTCCCCACTGATGCTCTGGGCGAGAGAGTGATGTGTCACTTCAACTGTGTGTAATA

4750

4770

4790

TGTCAGACACGTCCTACAATAACAGGCGTCATATTTGTATTATTTTGTAGTTTACTGTAGA

4810

4830

4850

AAATAATGTCACCGCCAAAGGTGATGAGAGTCACGTTTTGTAGGATCTGTTTTCTTATAC

4870

4890

4910

TTAAAGACAGACTTCTGCTACGGTAATTGCCAGTATTCATGGCTTCCTTTCTGTGTCAGA

4930

4950

4970

AGAGAAGGGATCTGCTTTCTCTGGCTGATTCACATAGCATTGGTAATAGACATGCATT

4990

5010

5030

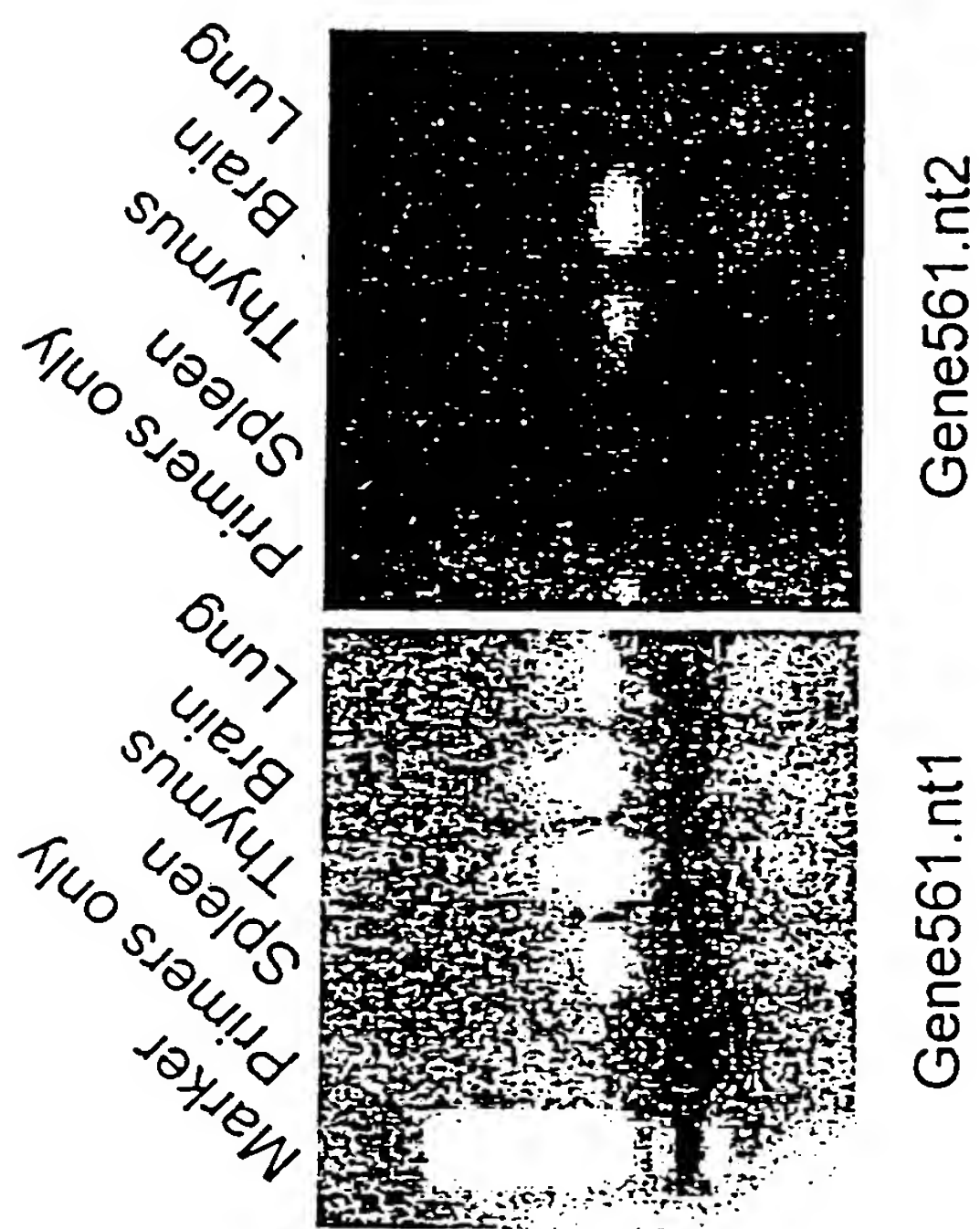
TCTCTTTCTAAAGGGGAGTAACTTTTAAACCCTTCCTGATTTTAGCCTGGCAATGTAAG

5050

5070

TGTCCTTAATGTGACTGTTTTGATAATTAAAAAAGGTATATAATTT

FIG. 7 H



RT/PCR of Gene561.nt1 and Gene561.nt2

FIG. 8

10	30	50
TCGAAACAGCTGCCGGCTGGTCCCGGCCGAGGCCGGCGCAGGGAGGGAGGAGCCGCCCGG		
70	90	110
GCTGTGGGGGCGCCGCGAGCTGGGCGCGCCTCGGTGTGCCCGCGCCGCCAGCCCGCTCCA		
130	150	170
GACGCGCCACCTGGGCGCTCCAAGAAGAGGCCGAAGTTTGCCGCGGCCGTGAGTTGGAGC		
190	210	230
TCGCGCCGGGCGCTGCGCCGGGAGCTCCGGGGGCTTCCCTCGCTTCCCGGTATTGTTTG		
250	270	290
CAAACCTTGCTGCTCTCCGCCGCGGCCCCCACTCGGCGGACGCCGGGCGCGGAGAGCCG		
310	330	350
AGCCGGGGGCGCTGTGCGCAGCGCTCGGGCCAGGCCGGGCGGGCATGGGCGGGGGCCCCGA		
370	390	410
GCAGGGGTGGAGAGCCGGGGCCAGCAGCAGCCCGTGCCCGGGAGCGGCGGCGCTGAGGGG		
430	450	470
CGCGGAGCTCCCCGCGAGGACACGTCCAACGCCAGCATGCAGCGCCCGGGCCCCCGCCTG		
		MetGlnArgProGlyProArgLeu
490	510	530
TGGCTGGTCCTGCAGGTGATGGGCTCGTGCGCCGCCATCAGCTCCATGGACATGGAGCGC		
		TrpLeuValLeuGlnValMetGlySerCysAlaAlaIleSerSerMetAspMetGluArg
550	570	590
CCGGGCGACGGCAAATGCCAGCCCATCGAGATCCCGATGTGCAAGGACATCGGCTACAAC		
		ProGlyAspGlyLysCysGlnProIleGluIleProMetCysLysAspIleGlyTyrAsn
610	630	650

FIG. 9 A



ATGACTCGTATGCCCAACCTGATGGGCCACGAGAACCAGCGCGAGGCAGCCATCCAGTTG  
MetThrArgMetProAsnLeuMetGlyHisGluAsnGlnArgGluAlaAlaIleGlnLeu

670

690

710

CACGAGTTCGCGCCGCTGGTGGAGTACGGCTGCCACGGCCACCTCCGCTTCTTCCTGTGC  
HisGluPheAlaProLeuValGluTyrGlyCysHisGlyHisLeuArgPhePheLeuCys

730

750

770

TCGCTGTACGCGCCGATGTGCACCGAGCAGGTCTCTACCCCCATCCCCGCCTGCCGGGTC  
SerLeuTyrAlaProMetCysThrGluGlnValSerThrProIleProAlaCysArgVal

790

810

830

ATGTGCGAGCAGGCCCGGCTCAAGTGCTCCCCGATTATGGAGCAGTTCAACTTCAAGTGG  
MetCysGluGlnAlaArgLeuLysCysSerProIleMetGluGlnPheAsnPheLysTrp

850

870

890

CCCGACTCCCTGGACTGCCGGAACTCCCCAACAAGAACGACCCCAACTACCTGTGCATG  
ProAspSerLeuAspCysArgLysLeuProAsnLysAsnAspProAsnTyrLeuCysMet

910

930

950

GAGGCGCCCAACAACGGCTCGGACGAGCCCACCCGGGGCTCGGGCCTGTTCCCGCCGCTG  
GluAlaProAsnAsnGlySerAspGluProThrArgGlySerGlyLeuPheProProLeu

970

990

1010

TTCCGGCCGCAGCGGCCCCACAGCGCGCAGGAGCACCCGCTGAAGGACGGGGGCCCCGGG  
PheArgProGlnArgProHisSerAlaGlnGluHisProLeuLysAspGlyGlyProGly

1030

1050

1070

CGCGGCGGCTGCGACAACCCGGGCAAGTTCCACCACGTGGAGAAGAGCGCGTCGTGCGCG  
ArgGlyGlyCysAspAsnProGlyLysPheHisHisValGluLysSerAlaSerCysAla

1090

1110

1130

CCGCTCTGCACGCCCGGCGTGGACGTGTACTGGAGCCGCGAGGACAAGCGCTTCGCAGTG  
ProLeuCysThrProGlyValAspValTyrTrpSerArgGluAspLysArgPheAlaVal

1150

1170

1190

FIG. 9 B

GTCTGGCTGGCCATCTGGGCGGTGCTGTGCTTCTTCTCCAGCGCCTTCACCGTGCTCACC  
ValTrpLeuAlaIleTrpAlaValLeuCysPhePheSerSerAlaPheThrValLeuThr

1210

1230

1250

TTCCTCATCGACCCGGCCCGCTTCCGCTACCCCGAGCGCCCATCATCTTCTCTCCATG  
PheLeuIleAspProAlaArgPheArgTyrProGluArgProIleIlePheLeuSerMet

1270

1290

1310

TGCTACTGCGTCTACTCCGTGGGCTACCTCATCCGCCTCTTCGCCGGCGCCGAGAGCATC  
CysTyrCysValTyrSerValGlyTyrLeuIleArgLeuPheAlaGlyAlaGluSerIle

1330

1350

1370

GCCTGCGACCGGGACAGCGGCCAGCTCTATGTCATCCAGGAGGGACTGGAGAGCACCGGC  
AlaCysAspArgAspSerGlyGlnLeuTyrValIleGlnGluGlyLeuGluSerThrGly

1390

1410

1430

TGCACGCTGGTCTTCCTGGTCCTCTACTACTTCGGCATGGCCAGCTCGCTGTGGTGGGTG  
CysThrLeuValPheLeuValLeuTyrTyrPheGlyMetAlaSerSerLeuTrpTrpVal

1450

1470

1490

GTCCTCACGCTCACCTGGTTCCTGGCCGCCGGCAAGAAGTGGGGCCACGAGGCCATCGAA  
ValLeuThrLeuThrTrpPheLeuAlaAlaGlyLysLysTrpGlyHisGluAlaIleGlu

1510

1530

1550

GCCAACAGCAGCTACTTCCACCTGGCAGCCTGGGCCATCCCGGCGGTGAAGACCATCCTG  
AlaAsnSerSerTyrPheHisLeuAlaAlaTrpAlaIleProAlaValLysThrIleLeu

1570

1590

1610

ATCCTGGTCATGCGCAGGGTGGCGGGGGACGAGCTCACCGGGGTCTGCTACGTGGGCAGC  
IleLeuValMetArgArgValAlaGlyAspGluLeuThrGlyValCysTyrValGlySer

1630

1650

1670

ATGGACGTCAACGCGCTCACCGGCTTCGTGCTCATTCCTGGCCTGCTACCTGGTCATC  
MetAspValAsnAlaLeuThrGlyPheValLeuIleProLeuAlaCysTyrLeuValIle

1690

1710

1730

FIG. 9 C

GGCACGTCCTTCATCCTCTCGGGCTTCGTGGCCCTGTTCCACATCCGGAGGGTGATGAAG  
GlyThrSerPheIleLeuSerGlyPheValAlaLeuPheHisIleArgArgValMetLys

1750

1770

1790

ACGGGCGGGCGAGAACACGGACAAGCTGGAGAAGCTCATGGTGCGTATCGGGCTCTTCTCT  
ThrGlyGlyGluAsnThrAspLysLeuGluLysLeuMetValArgIleGlyLeuPheSer

1810

1830

1850

GTGCTGTACACCGTGCCGGCCACCTGTGTGATCGCCTGCTACTTTTACGAACGCCTCAAC  
ValLeuTyrThrValProAlaThrCysValIleAlaCysTyrPheTyrGluArgLeuAsn

1870

1890

1910

ATGGATTACTGGAAGATCCTGGCGGCGCAGCACAAGTGCAAAATGAACAACCAGACTAAA  
MetAspTyrTrpLysIleLeuAlaAlaGlnHisLysCysLysMetAsnAsnGlnThrLys

1930

1950

1970

ACGCTGGACTGCCTGATGGCCGCCTCCATCCCCGCCGTGGAGATCTTCATGGTGAAGATC  
ThrLeuAspCysLeuMetAlaAlaSerIleProAlaValGluIlePheMetValLysIle

1990

2010

2030

TTTATGCTGCTGGTGGTGGGGATCACCAGCGGGATGTGGATTTGGACCTCCAAGACTCTG  
PheMetLeuLeuValValGlyIleThrSerGlyMetTrpIleTrpThrSerLysThrLeu

2050

2070

2090

CAGTCCTGGCAGCAGGTGTGCAGCCGTAGGTTAAAGAAGAAGAGCCGGAGAAAACCGGCC  
GlnSerTrpGlnGlnValCysSerArgArgLeuLysLysLysSerArgArgLysProAla

2110

2130

2150

AGCGTGATCACCAGCGGTGGGATTTACAAAAAGCCCAGCATCCCCAGAAAACCTCACCAC  
SerValIleThrSerGlyGlyIleTyrLysLysAlaGlnHisProGlnLysThrHisHis

2170

2190

2210

GGGAAATATGAGATCCCTGCCCAGTCGCCCACCTGCGTGTGAACAGGGCTGGAGGGAAGG  
GlyLysTyrGluIleProAlaGlnSerProThrCysValEnd

2230

2250

2270

FIG. 9 D

GCACAGGGGCGCCCGGAGCTAAGATGTGGTGTCTTTCTTGGTTGTGTTTTCTTTCTTCT

2290

2310

2330

TCTTCTTTTTTTTTTTTTTATAAAAGCAAAGAGAAATACATAAAAAAGTGTTACCCTG

2350

2370

2390

AAATTCAGGATGCTGTGATACACTGAAAGGAAAATGTACTTAAAGGGTTTTGTTTTGTT

2410

2430

2450

TTGGTTTTCCAGCGAAGGGAAGCTCCTCCAGTGAAGTAGCCTCTTGTGTAACTAATTTGT

2470

2490

2510

GGTAAAGTAGTTGATTCAGCCCTCAGAAGAAACTTTTGTTTAGAGCCCTCCSTAAATAT

2530

2550

2570

ACATCTGTGTATTTGAGTTGGCTTTGCTACCCATTTACAAATAAGAGGACAGATAACTGC

2590

2610

2630

TTTGCAAATTCAGAGCCTCCCCTGGGTAAACAAATGAGCCATCCCCAGGGCCCACCCCC

2650

2670

2690

AGGAAGGCCACAGTGCTGGGCGGCATCCCTGCAGAGGAAAGACAGGACCCGGGGCCCGCC

2710

2730

2750

TCACACCCCAGTGGATTTGGAGTTGCTTAAATAGACTCCGGCCTTCACCAATAGTCTCT

2770

2790

2810

CTGCAAGACAGAAACCTCCATCAAACCTCACATTTGTGAACTCAAACGATGTGCAATACA

2830

2850

2870

TTTTTTCTCTTTCCTTGAAAATAAAAAGAGAAACAAGTATTTTGCTATATATAAGACA

2890

2910

2930

FIG. 9 E

ACAAAAGAAATCTCCTAACAAAAGAACTAAGAGGCCCCAGCCCTCAGAAACCCTTCAGTGC

2950

2970

2990

TACATTTTGTGGCTTTTAAATGGAAACCAAGCCAATGTTATAGACGTTTGGACTGATTG

3010

3030

3050

TGGAAAGGAGGGGGGAAGAGGGAGAAGGATCATTCAAAGTTACCCAAAGGGCTTATTGA

3070

3090

3110

CTCTTTCTATTGTTAAACAAATGATTTCCACAAACAGATCAGGAAGCACTAGGTTGGCAG

3130

3150

3170

AGACACTTTGTCTAGTGTATTCTCTTCACAGTGCCAGGAAGAGTGGTTTCTGCGTGTGT

3190

3210

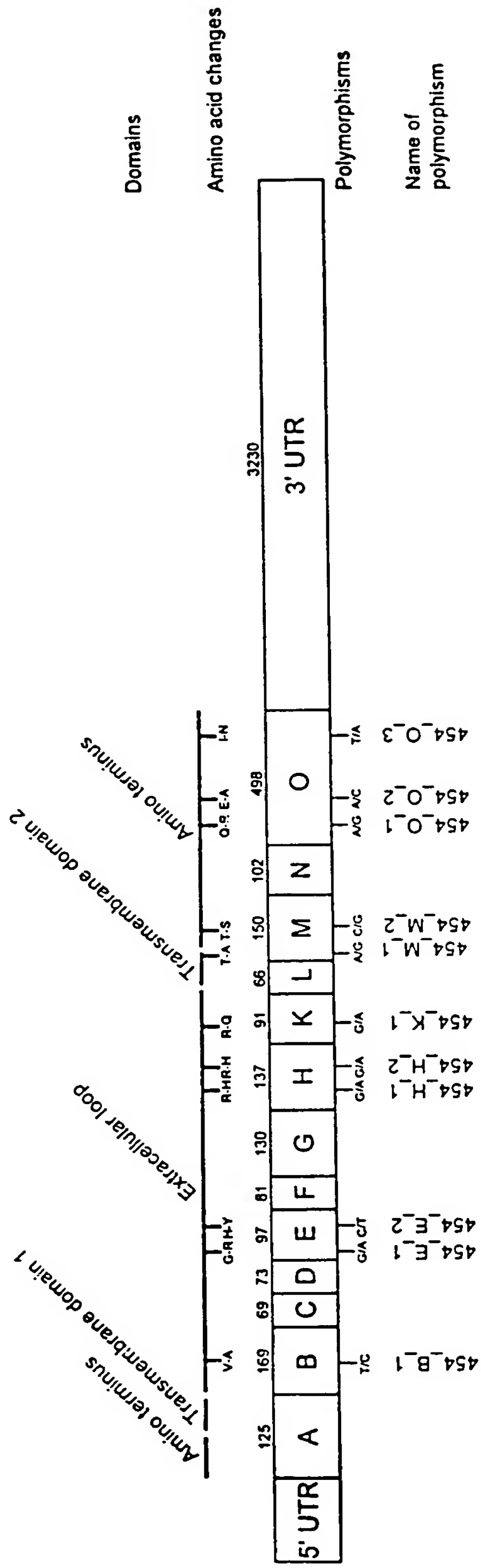
3230

ATATTTGTAATATATGATATTTTTCATGCTCCACTATTTTATTAAAAATAAAATATGTTT

3250

TTTAGTTTGCTGCT

FIG. 9 F



Location of SNPs/Amino Acid Changes/Domain within the Transcript of Gene 454

FIG. 10

Manhattan plot showing the association of various SNPs with gene expression. The y-axis represents  $-\log_{10}(\text{p-value})$  (ranging from 0.0 to 2.5), and the x-axis represents Location in kb (ranging from 4000 to 12000). Two horizontal dotted lines indicate significance thresholds at  $p=0.005$  and  $p=0.05$ .

Legend for gene names and symbols:

- gene 454:  $\Delta$
- gene 436:  $\boxtimes$
- gene 515:  $\boxplus$
- gene 570:  $\circ$
- gene 757:  $+$
- gene 698:  $\diamond$
- gene 561:  $\blacktriangle$
- gene 581:  $*$
- gene 722:  $\oplus$
- gene 702:  $\blacksquare$
- gene 214:  $\nabla$

Key SNPs and their approximate locations and  $-\log_{10}(\text{p-value})$  values:

- $\Delta M_1$ : ~4000 kb,  $-\log_{10}(\text{p-value}) \approx 2.4$
- $\Delta E_2$ : ~4500 kb,  $-\log_{10}(\text{p-value}) \approx 2.2$
- $\Delta M_1$ : ~4800 kb,  $-\log_{10}(\text{p-value}) \approx 2.1$
- $\Delta F_2$ : ~5000 kb,  $-\log_{10}(\text{p-value}) \approx 2.0$
- $\Delta M_1$ : ~5500 kb,  $-\log_{10}(\text{p-value}) \approx 1.9$
- $\Delta O_6$ : ~6000 kb,  $-\log_{10}(\text{p-value}) \approx 1.7$
- $\Delta O_1$ : ~6500 kb,  $-\log_{10}(\text{p-value}) \approx 1.6$
- $\Delta L_1$ : ~7000 kb,  $-\log_{10}(\text{p-value}) \approx 1.1$
- $\Delta V_1$ : ~7500 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta H_1$ : ~7800 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta E_1$ : ~8000 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta J_1$ : ~8500 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $E_1$ : ~9000 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta V_1$ : ~9500 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta V_1$ : ~10000 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta V_1$ : ~10500 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta V_1$ : ~11000 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta V_1$ : ~11500 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$
- $\Delta V_1$ : ~12000 kb,  $-\log_{10}(\text{p-value}) \approx 1.0$

**FIG. 11**

# Chr. 12 Case(Asthma)/Control: Alleles

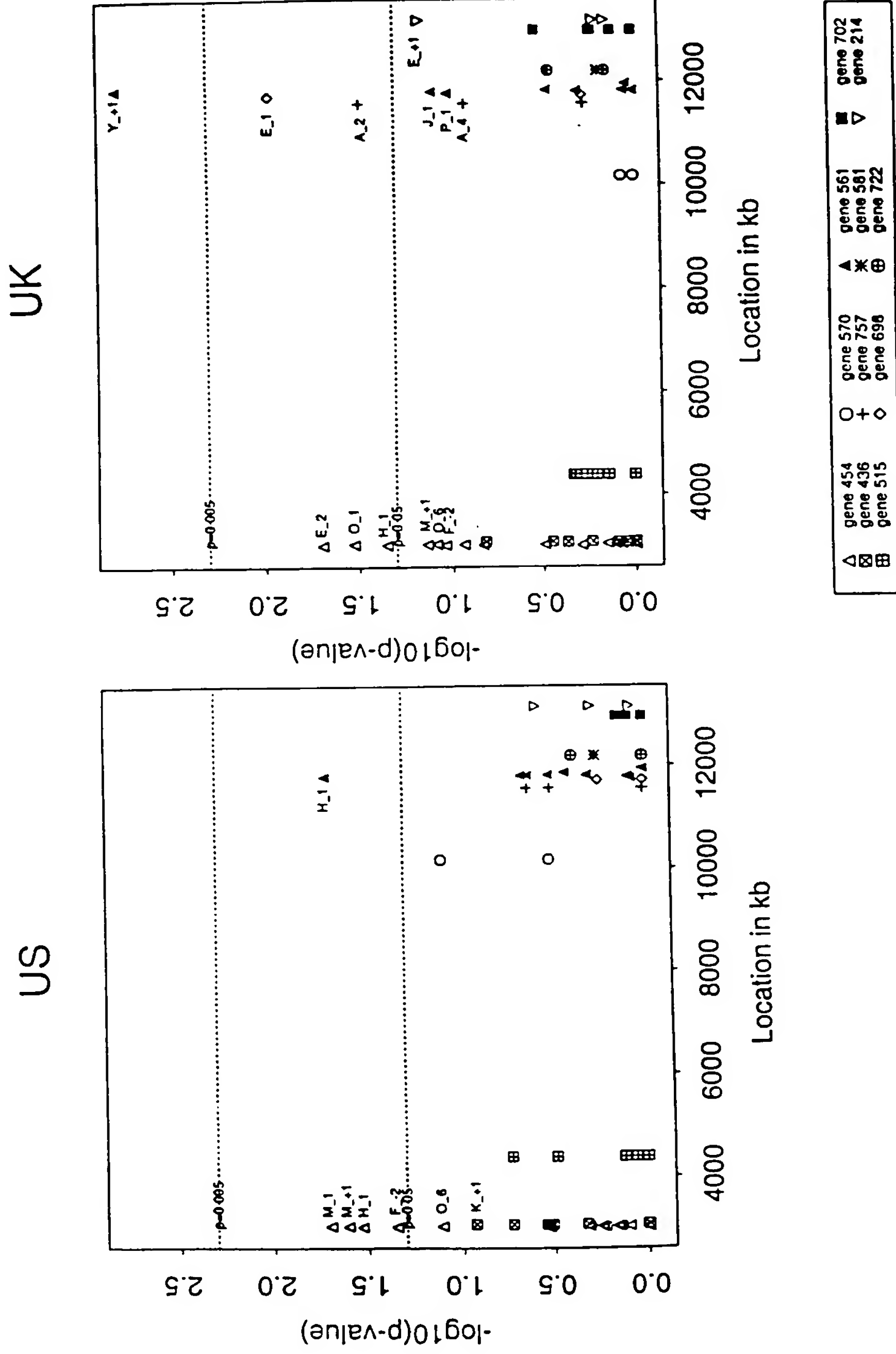


FIG. 12



Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Alleles

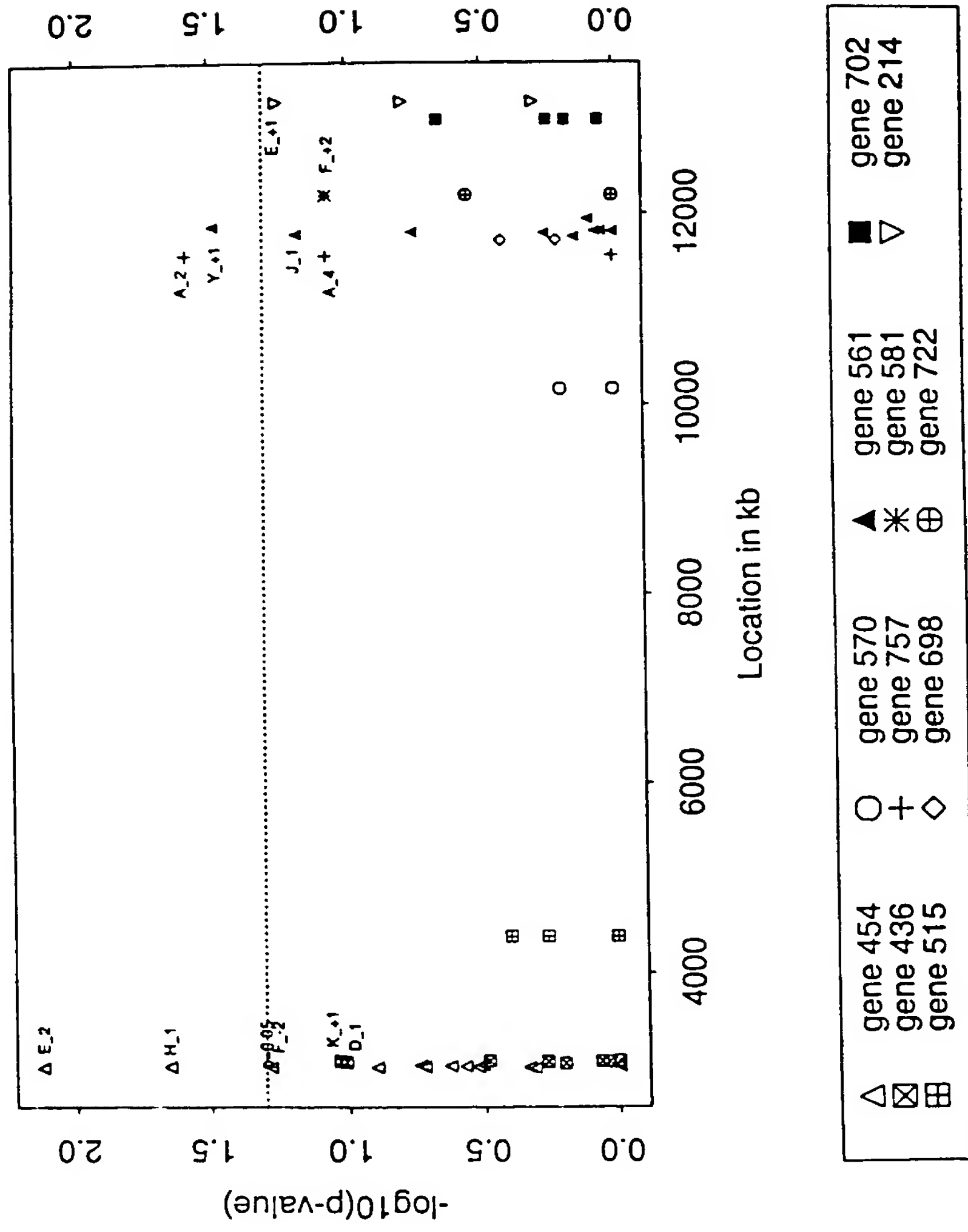


FIG. 13

Chr. 12 Case(BHR (PC20  $\leq$  16 mg/ml) & Asthma)/Control: Alleles

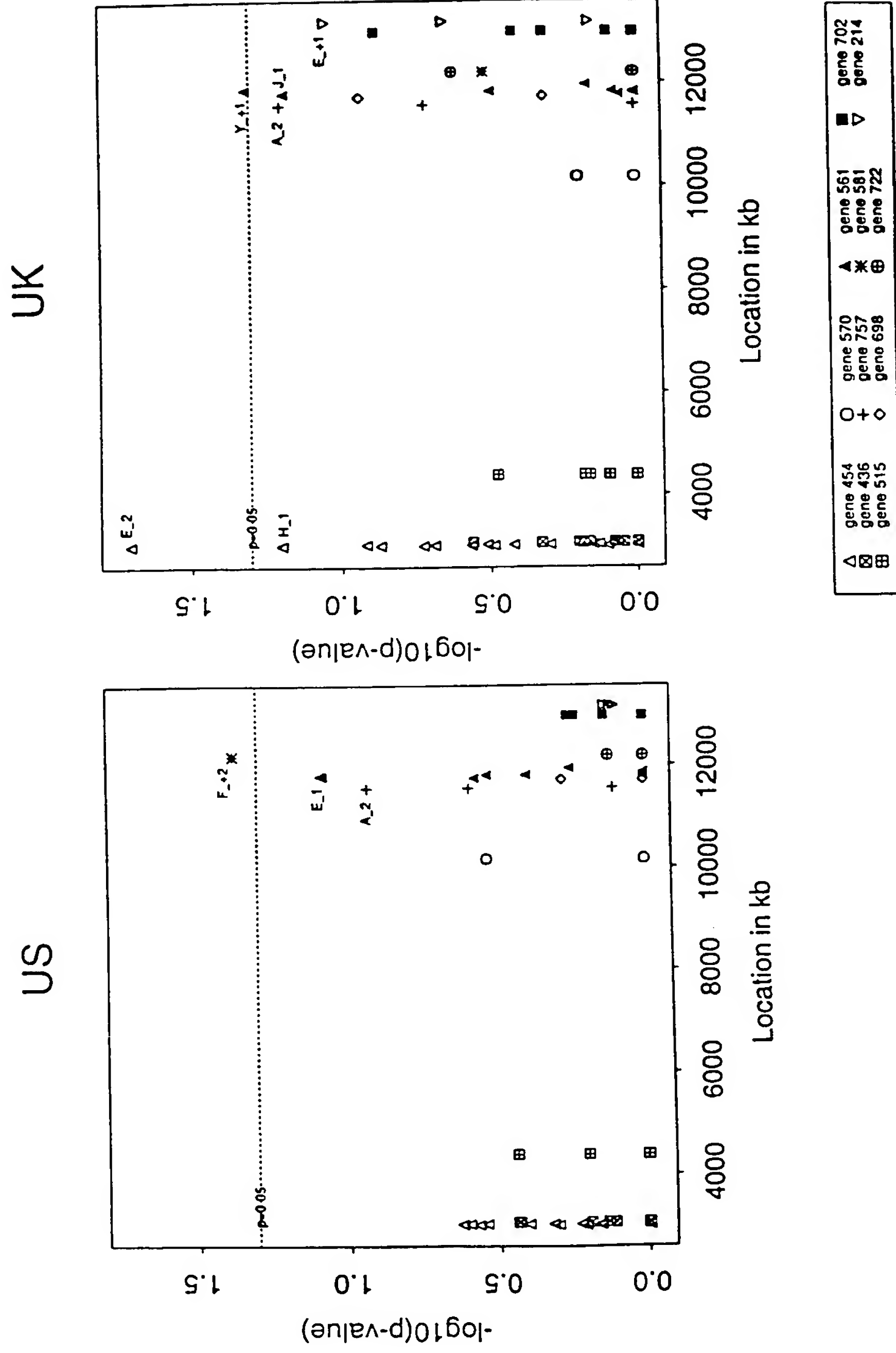


FIG. 14

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

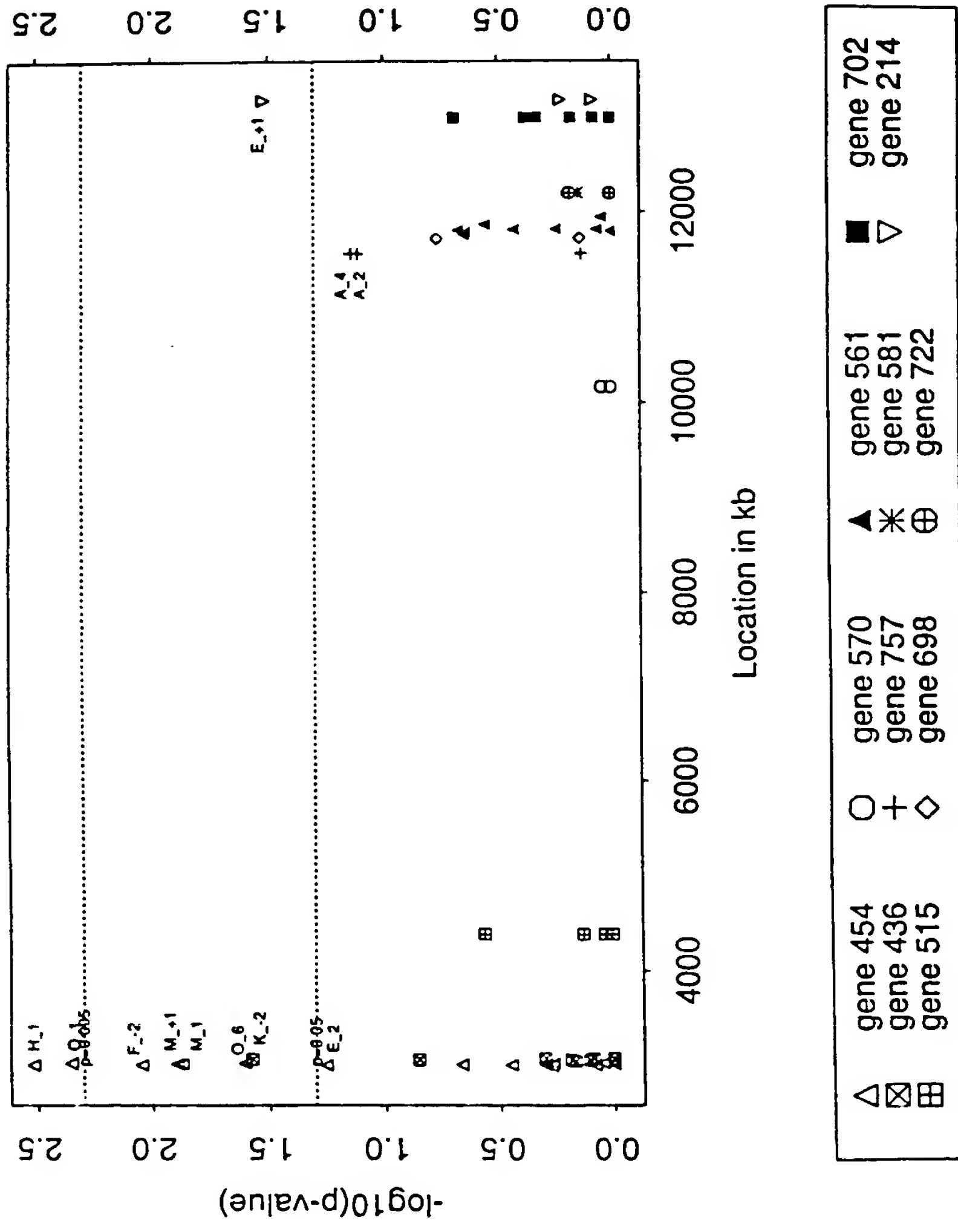


FIG. 15

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

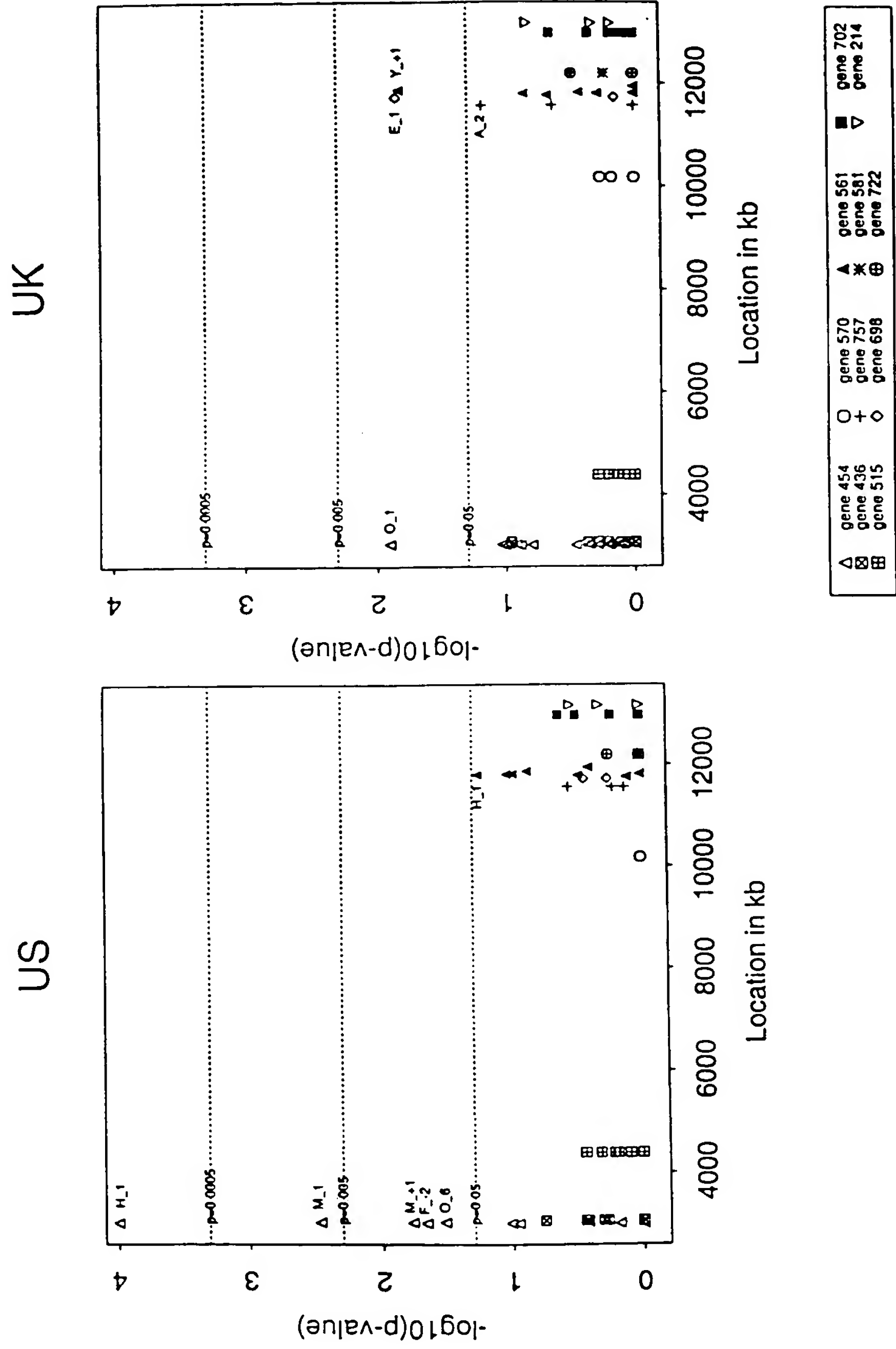


FIG. 16

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

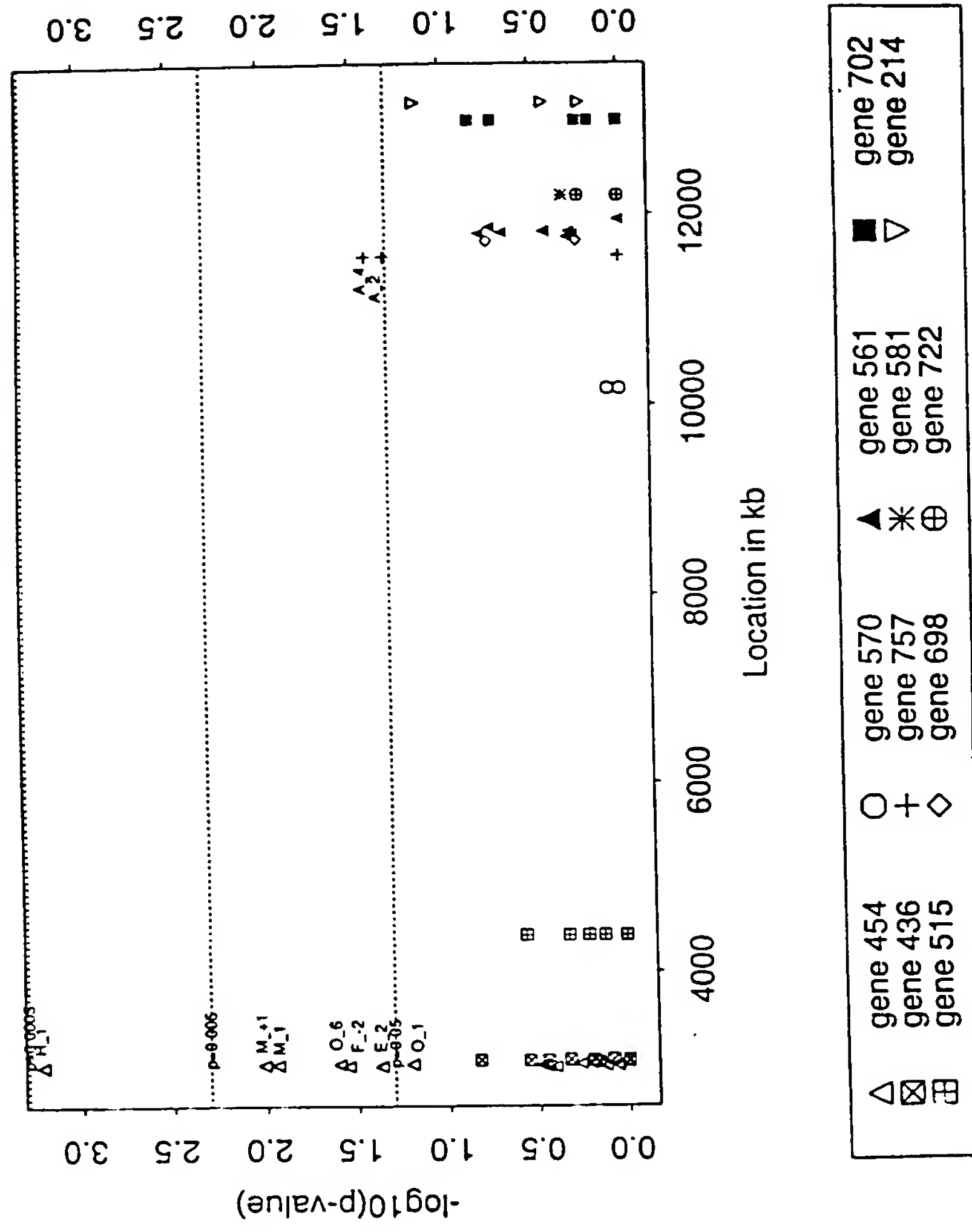


FIG. 17

# Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

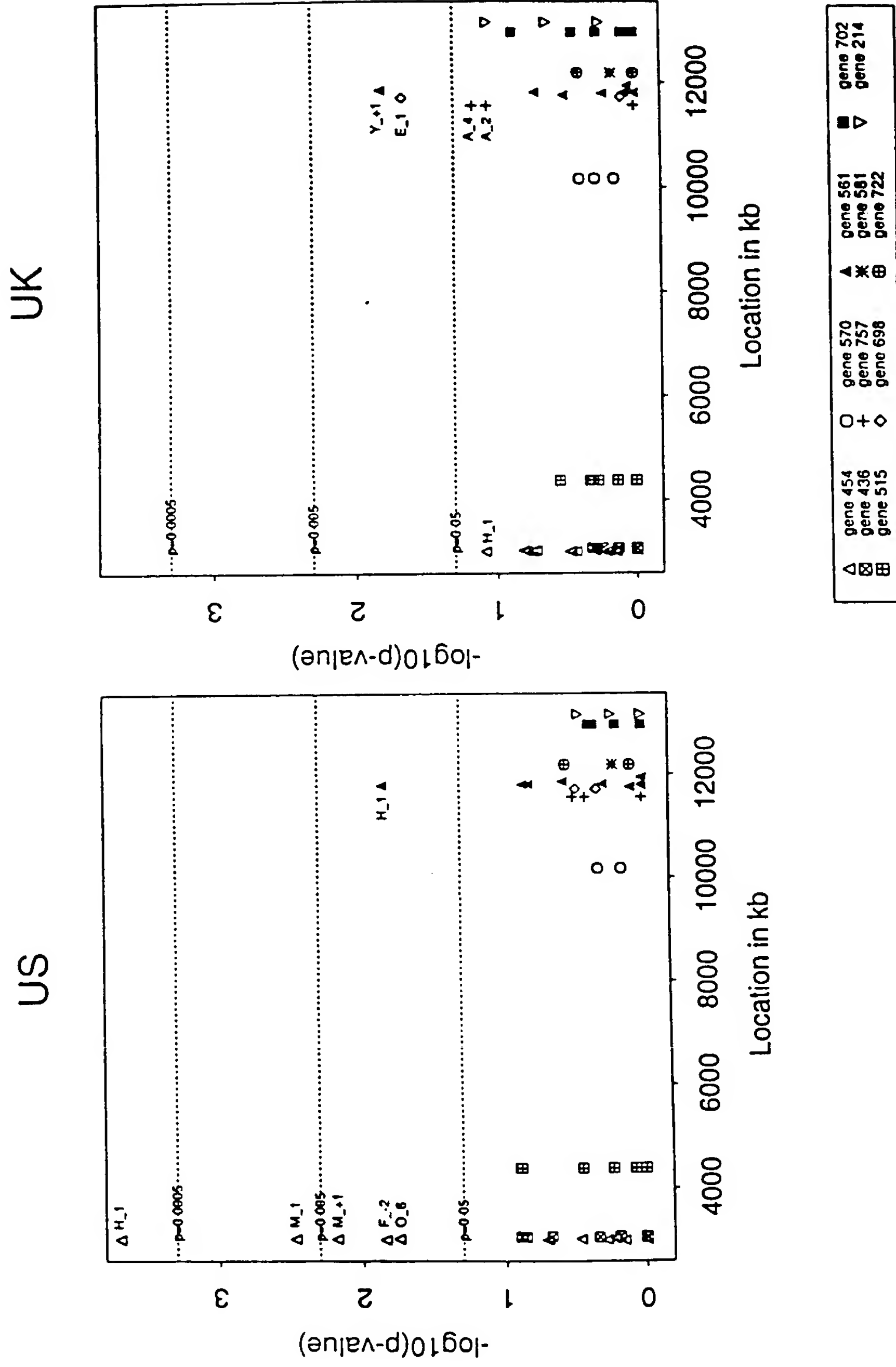


FIG. 18

Manhattan plot showing the association of various genes with the trait 214\_E-1\_E-1\_V. The y-axis represents  $-\log_{10}(\text{p-value})$  (ranging from 0 to 4), and the x-axis represents the Averaged Location in kb (ranging from 0 to 12000). A significant peak is observed around 11000 kb, reaching a  $-\log_{10}(\text{p-value})$  of approximately 3.5. The plot includes a legend for various gene symbols and a list of genes: gene 454, gene 436, gene 515, gene 570, gene 757, gene 698, gene 561, gene 722, gene 702, and gene 214. The plot also shows a horizontal line at  $p=0.0001$  and a vertical line at 4000 kb.



# Chr. 12 Case(Asthma)/Control: Haplotype

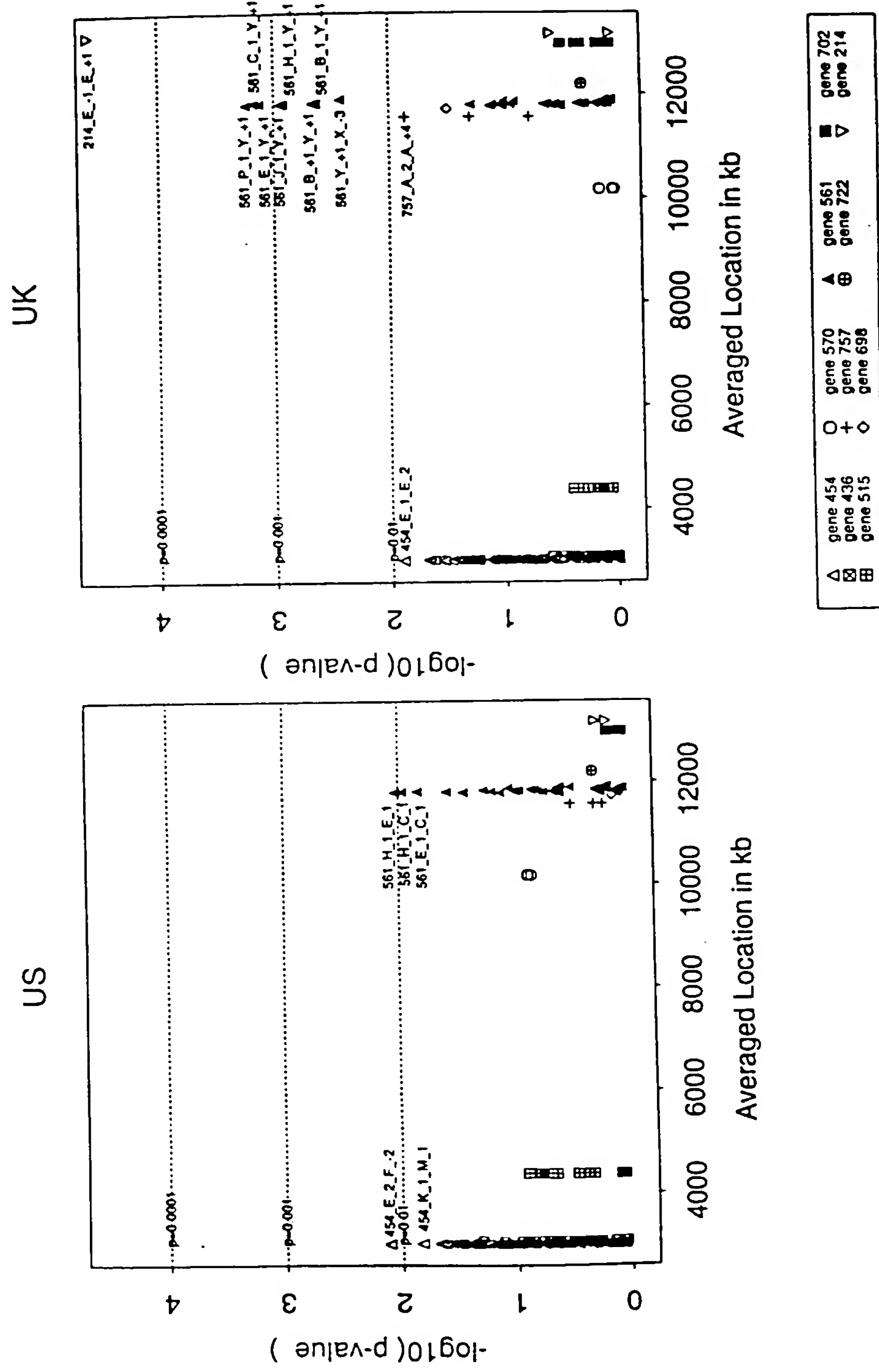


FIG. 20

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

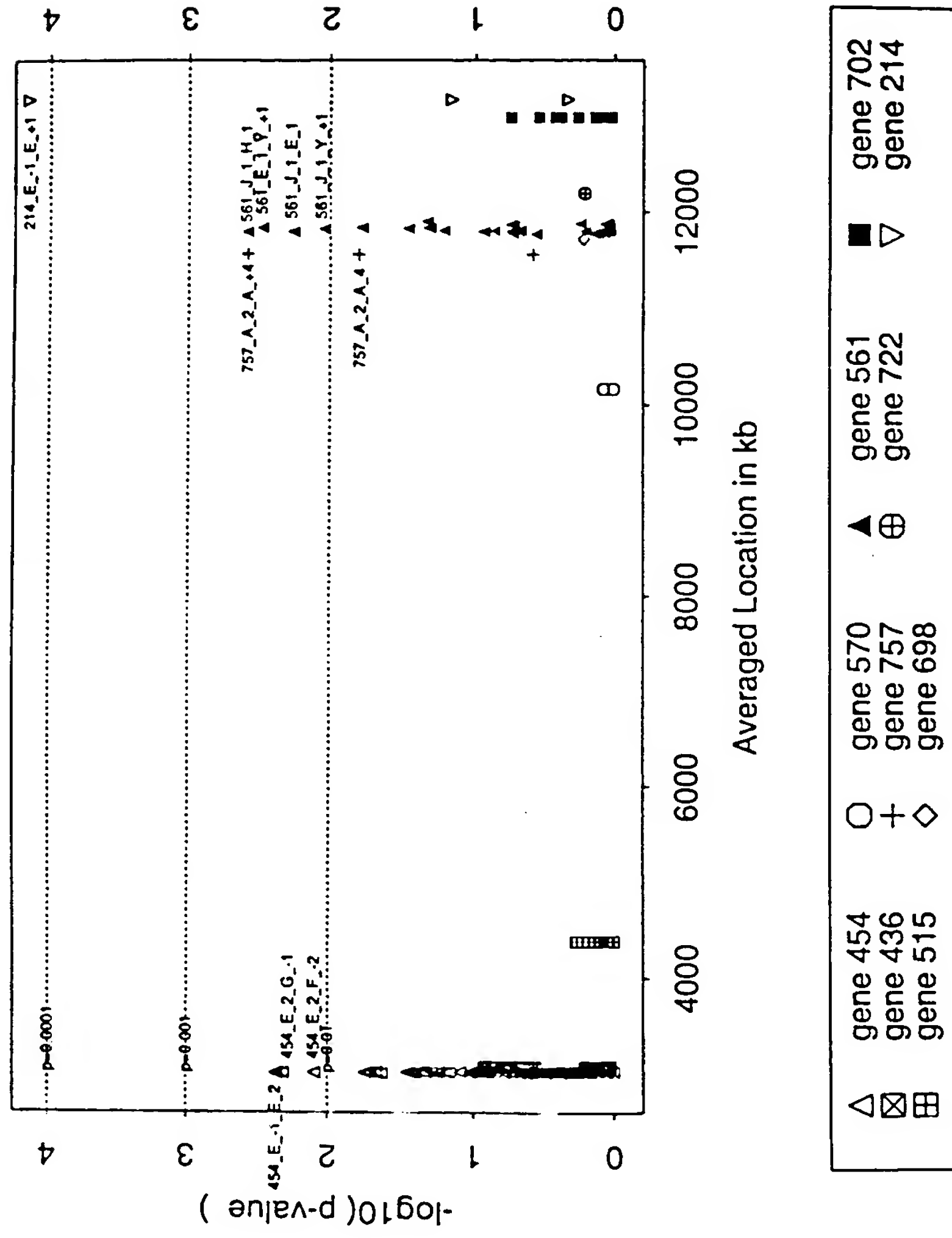


FIG. 21

Chr. 12 Case(BHR (PC20  $\leq$  16 mg/ml) & Asthma)/Control: Haplotype

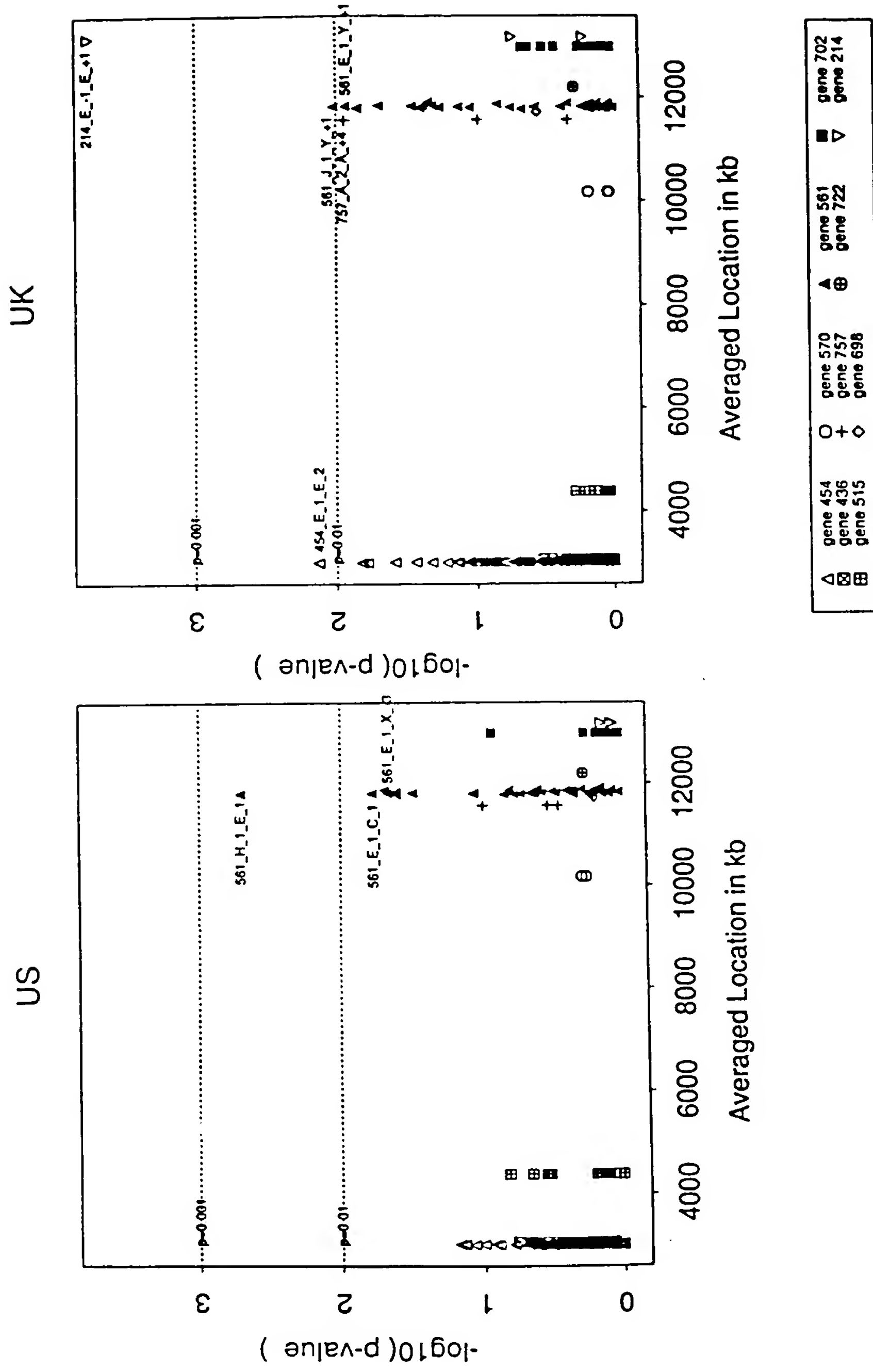


FIG. 22

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

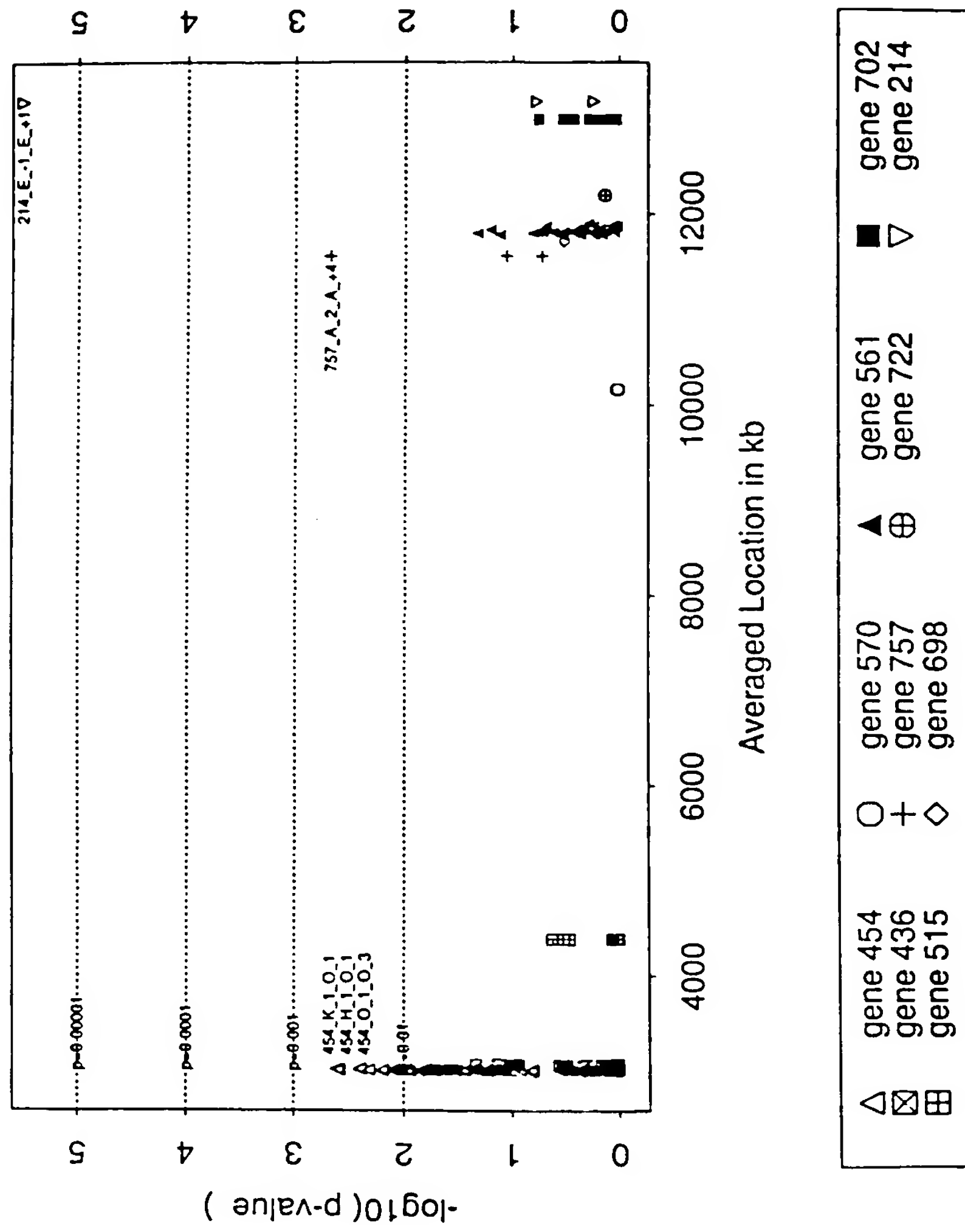


FIG. 23

# Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

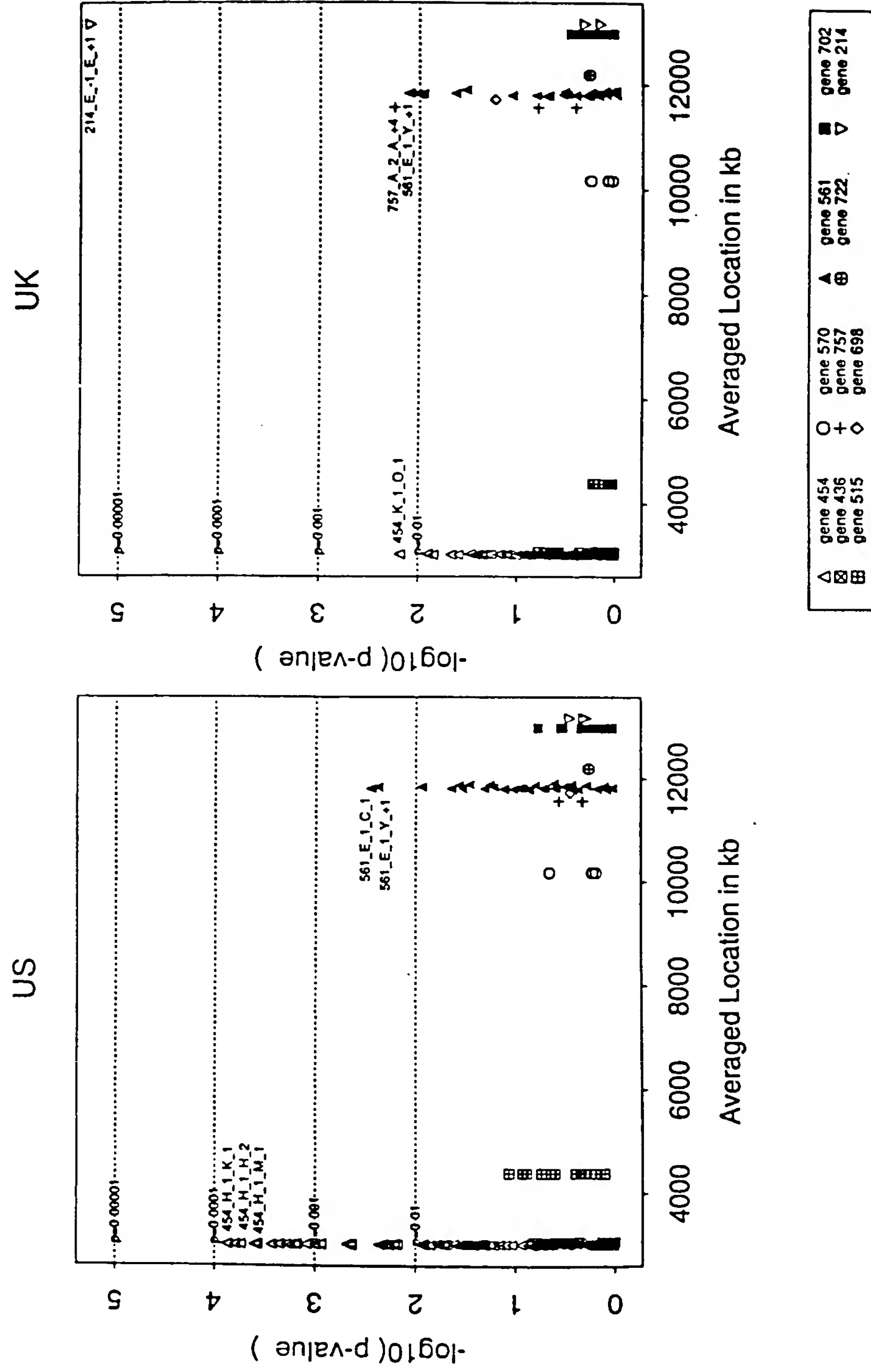


FIG. 24

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

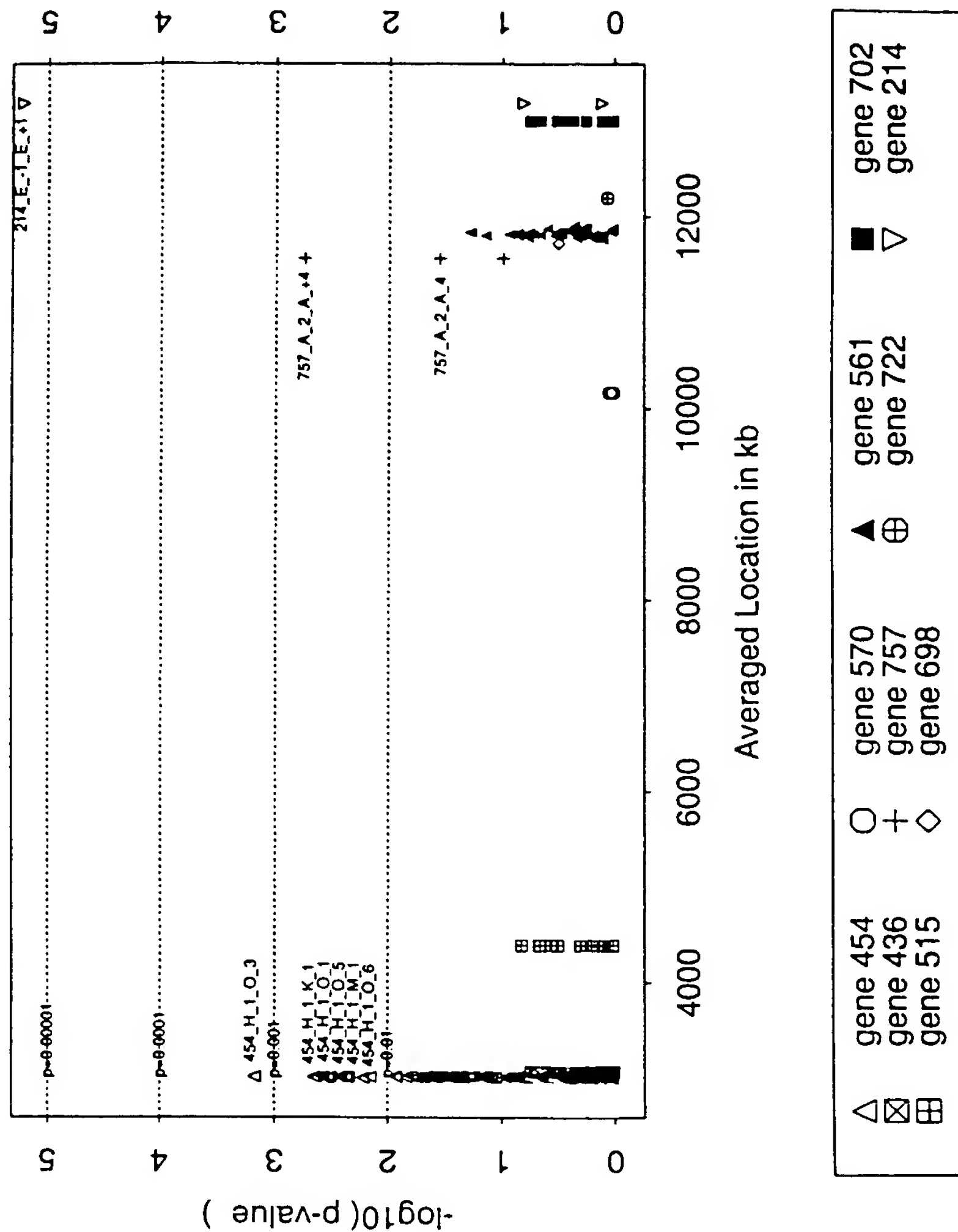


FIG. 25

# Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

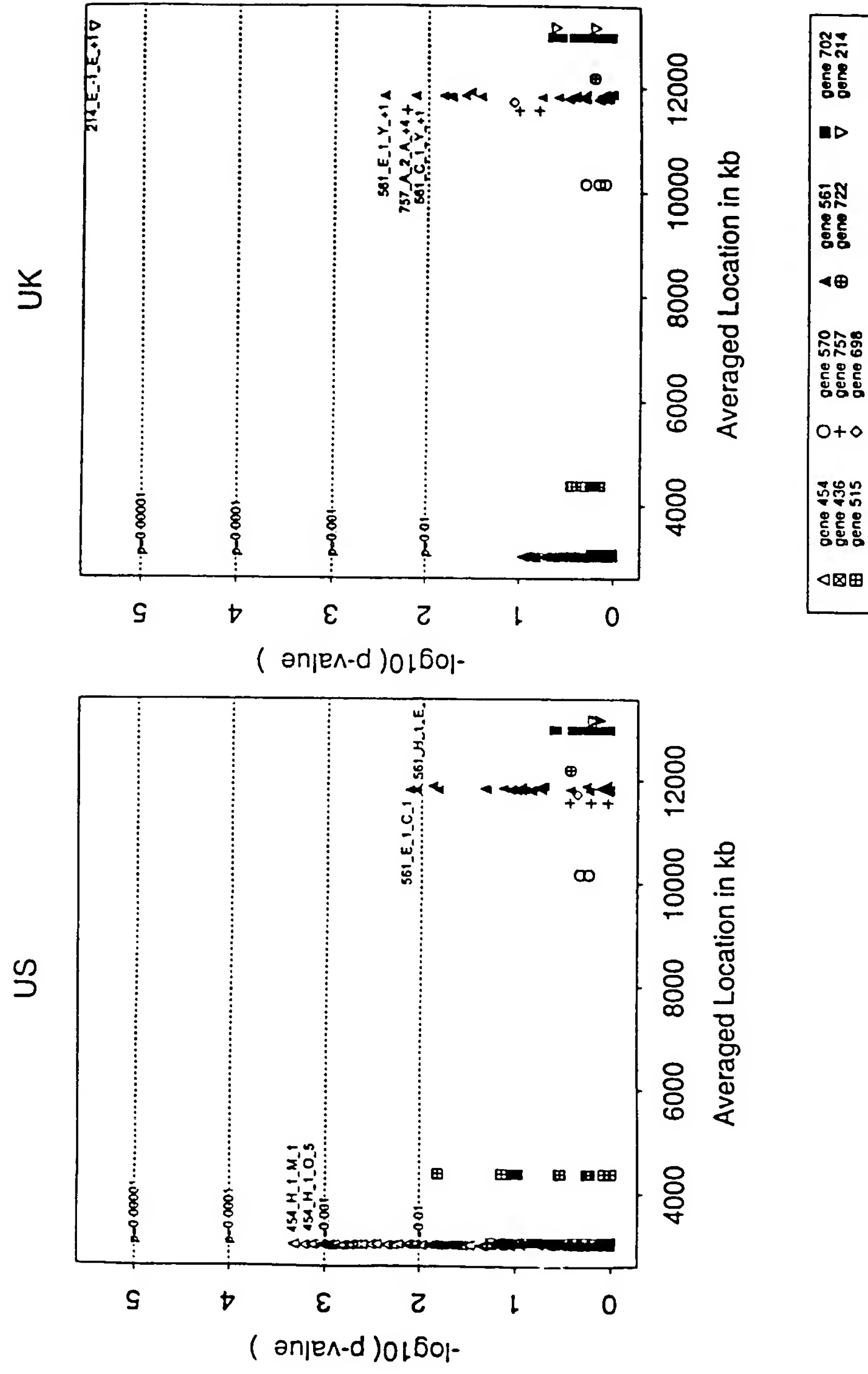


FIG. 26



10 30 50  
 CTTGGAATGACCCGCCACACCTGAAGCCTGCAGGTGCTGAGGCCACATTCGATCAGACC  
 70 90 110  
 CAAGCTTTGGGAGACCGCTGGGGAAATTTCCCACTTCCTCTCCTGAGACCAGGAACTCAG  
 130 150 170  
 CAGAGAACTTTGTGGAAAATGAACTGAAGGATGCCACCCAGGGAGAGTATCTCCTGAGA  
 190 210 230  
 TCCCATCATGCAGGCCTTCCACAAGGGCCCGGCAGCATGACAAGGTGAAGGCAGAGTAT  
 250 270 290  
 GTGCATCTCAACCAYCCGCTCACCCCTCGTGACCAGAGAGCGCGATTGCGCCGTGAAGGAG  
 310 330 350  
 AAACACCAGCTCCAAGCCAAGCTGGAGAACCTAGAACAGGTCCTGAAGCATATGCGAGAG  
 MetArgGlu  
 370 390 410  
 GCGGCTGAACGGCGGCAGCAGCTGCAGTTGGAGCATGACCAGGCCCTGGCTGTTCTCAGT  
 AlaAlaGluArgArgGlnGlnLeuGlnLeuGluHisAspGlnAlaLeuAlaValLeuSer  
 430 450 470  
 GCCAAGCAGCAGGAAATTGACCTTCTGCAGAAGTCCAAGGTTTCGAGAGCTGGAAGAGAAA  
 AlaLysGlnGlnGluIleAspLeuLeuGlnLysSerLysValArgGluLeuGluGluLys  
 490 510 530  
 TGCCGGACTCAAAGTGAGCAGTTCAACCTGCTGTCCCGGGACCTGGAGAAGTTCCGGCAG  
 CysArgThrGlnSerGluGlnPheAsnLeuLeuSerArgAspLeuGluLysPheArgGln  
 550 570 590  
 CACGCTGGCAAGATTGACCTGCTGGGTGGCAGCGCGGTGGCCCCCTGGACATCTCCACG  
 HisAlaGlyLysIleAspLeuLeuGlyGlySerAlaValAlaProLeuAspIleSerThr

FIG. 27 A

610	630	650
G C C C C C A G C A A G C C T T T C C C A C A G T T C A T G A A T G G C C T A G C C A C C T C C C T C G G C A A A G G T AlaProSerLysProPheProGlnPheMetAsnGlyLeuAlaThrSerLeuGlyLysGly		
670	690	710
C A G G A G A G C G C T A T T G G A G G C A G C T C T G C G A T C G G T G A A T A T A T C C G G C C C C T T C C G C A G GlnGluSerAlaIleGlyGlySerSerAlaIleGlyGluTyrIleArgProLeuProGln		
730	750	770
C C T G G T G A C A G G C C G G A G C C T C T G T C C G C C A A G C C C A C C T T C C T G T C G A G A T C C G G T A G C ProGlyAspArgProGluProLeuSerAlaLysProThrPheLeuSerArgSerGlySer		
790	810	830
G C A A G A T G C A G A T C T G A G T C A G A C A T G G A G A A T G A A C G G A A T T C C A A T A C C T C C A A G C A G AlaArgCysArgSerGluSerAspMetGluAsnGluArgAsnSerAsnThrSerLysGln		
850	870	890
A G A T A C T C G G G G A A G G T C C A C C T C T G T G T T G C C C G C T A T A G T T A C A A C C C C T T C G A T G G A ArgTyrSerGlyLysValHisLeuCysValAlaArgTyrSerTyrAsnProPheAspGly		
910	930	950
C C G A A C G A G A A C C C C G A A G C T G A G C T G C C C C T C A C G G C G G G A A A A T A C C T C T A C G T C T A T ProAsnGluAsnProGluAlaGluLeuProLeuThr <u>Ala</u> GlyLysTyrLeuTyrValTyr		
970	990	1010
G G A G A C A T G G A T G A G G A T G G G T T C T A T G A A G G A G A G C T C C T C G A T G G C C A G A G G G G T C T G GlyAspMetAspGluAspGlyPheTyrGluGlyGluLeuLeuAspGlyGlnArgGlyLeu		
1030	1050	1070
G T G C C C T C C A A C T T C G T G G A C T T T G T G C A G G A C A A C G A G T C G C G G T T G G C A A G C A C G C T G ValProSerAsnPheValAspPheValGlnAspAsnGluSerArgLeuAlaSerThrLeu		
1090	1110	1130
G G G A A C G A G C A G G A T C A G A A C T T C A T C A A C C A T T C C G G C A T C G G C C T G G A G G G A G A G C A C GlyAsnGluGlnAspGlnAsnPheIleAsnHisSerGlyIleGlyLeuGluGlyGluHis		
1150	1170	1190
A T C C T G G A C C T C C A C T C C C C A A C C C A C A T A G A T G C G G G C A T C A C C G A C A A C A G T G C C G G G		

FIG. 27 B

IleLeuAspLeuHisSerProThrHisIleAspAlaGlyIleThrAspAsnSerAlaGly

1210

1230

1250

ACCCTGGACGTGAACATCGACGACATCGGAGAAGACATCGTGCCTTACCCTAGAAAAATC  
ThrLeuAspValAsnIleAspAspIleGlyGluAspIleValProTyrProArgLysIle

1270

1290

1310

ACCCTCATCAAACAACTCGCCAAAAGTGTATTGTGGGCTGGGAGCCCCCGGCGGTGCCA  
ThrLeuIleLysGlnLeuAlaLysSerValIleValGlyTrpGluProProAlaValPro

1330

1350

1370

CCAGGATGGGGAACGGTGAGCAGCTACAACGTCCTGGTGGACAAGGAGACACGCATGAAC  
ProGlyTrpGlyThrValSerSerTyrAsnValLeuValAspLysGluThrArgMetAsn

1390

1410

1430

CTCACGCTGGGGAGCAGAACTAAAGCCCTCATCGAGAAGCTCAACATGGCAGCCTGCACC  
LeuThrLeuGlySerArgThrLysAlaLeuIleGluLysLeuAsnMetAlaAlaCysThr

1450

1470

1490

TACCGCATCTCCGTGCAGTGCGTCACCAGCAGGGGCAGCTCGGATGAGCTGCAGTGCACG  
TyrArgIleSerValGlnCysValThrSerArgGlySerSerAspGluLeuGlnCysThr

1510

1530

1550

CTGCTGGTGGGCAAGGACGTGGTGGTGGCCCCCTCCCACCTGCGGGTGGACAACATCACG  
LeuLeuValGlyLysAspValValValAlaProSerHisLeuArgValAspAsnIleThr

1570

1590

1610

CAGATCTCCGCCCAGCTCTCCTGGCTACCCACCAACAGCAACTACAGCCACGTCATCTTC  
GlnIleSerAlaGlnLeuSerTrpLeuProThrAsnSerAsnTyrSerHisValIlePhe

1630

1650

1670

CTCAACGAGGAGGAGTTCGACATCGTCAAGGCCGCCAGGTACAAGTACCAGTTCTTCAAT  
LeuAsnGluGluGluPheAspIleValLysAlaAlaArgTyrLysTyrGlnPhePheAsn

1690

1710

1730

CTCAGGCCCAACATGGCCTATAAGGTGAAGGTTCTGGCCAAACCCACCAAGATGCCGTGG  
LeuArgProAsnMetAlaTyrLysValLysValLeuAlaLysProHisGlnMetProTrp

FIG. 27 C

1750	1770	1790
CAGCTCCCGCTGGAGCAAAGGGAGAAGAAGGAGGCCTTTGTGGAGTTCTCCACGTTGCCT GlnLeuProLeuGluGlnArgGluLysLysGluAlaPheValGluPheSerThrLeuPro		
1810	1830	1850
GCAGGACCCCCAGCACCCCCACAAGATGTTACCGTCCAGGCTGGGGTGACCCCCGCCACC AlaGlyProProAlaProProGlnAspValThrValGlnAlaGlyValThrProAlaThr		
1870	1890	1910
ATCCGGGTCTCCTGGAGACCACCTGTGCTGACGCCACCGGGCTGTCCAATGGCGCAAAC IleArgValSerTrpArgProProValLeuThrProThrGlyLeuSerAsnGlyAlaAsn		
1930	1950	1970
GTTACCGGCTACGGCGTGTATGCCAAAGGGCAGAGGGTGGCTGAAGTCATCTTCCCCACG ValThrGlyTyrGlyValTyrAlaLysGlyGlnArgValAlaGluValIlePheProThr		
1990	2010	2030
GCAGACAGCACGGCCGTGGAGCTTGTGCGGCTGCGGAGCCTGGAGGCCAAGGGCGTGACC AlaAspSerThrAlaValGluLeuValArgLeuArgSerLeuGluAlaLysGlyValThr		
2050	2070	2090
GTGCGGACCCTCTCCGCCCAGGGCGAGTCCGTGGACTCTGCAGTTGCTGCCGTTCCCCC ValArgThrLeuSerAlaGlnGlyGluSerValAspSerAlaValAlaAlaValProPro		
2110	2130	2150
GAGCTCCTGGTGCCTCCTACCCCCACCCGAGACCTGCACCCCAATCAAAGCCATTAGCA GluLeuLeuValProProThrProHisProArgProAlaProGlnSerLysProLeuAla		
2170	2190	2210
AGTTCTGGAGTCCCCGAAACCAAAGACGAGCACCTGGGTCCCCACGCCAGGATGGATGAG SerSerGlyValProGluThrLysAspGluHisLeuGlyProHisAlaArgMetAspGlu		
2230	2250	2270
GCCTGGGAGCAGAGCCGTGCACCTGGCCCTGTGCATGGGCACATGCTGGAGCCGCCCGTG AlaTrpGluGlnSerArgAlaProGlyProValHisGlyHisMetLeuGluProProVal		
2290	2310	2330
GGCCCCGGAAGGCGGTGCGCCCTCACCCAGCCGCATCCTGCCGCAGCCACAGGGCACCCCCG		

FIG. 27 D

GlyProGlyArgArgSerProSerProSerArgIleLeuProGlnProGlnGlyThrPro

2350

2370

2390

GTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCCGAGAGC  
ValSerThrThrValAlaLysAlaMetAlaArgGluAlaAlaGlnArgValAlaGluSer

2410

2430

2450

AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGCGGGGCAGTACGCCGCC  
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

2470

2490

2510

TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC  
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

2530

2550

2570

GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGCCGCACTGTTGCCATGGAGACGAGTAC  
AspPheLeuLysGlySerGluLeuGlyLysGlnProHisCysCysHisGlyAspGluTyr

2590

2610

2630

CACACAGAGAGCAGCCGGGGGTCTGACCTCTCAGACATCATGGAGGAGGACGAGGAGGAG  
HisThrGluSerSerArgGlySerAspLeuSerAspIleMetGluGluAspGluGluGlu

2650

2670

2690

CTGTATTCTGAAATGCAGCTGGAAGATGGGGGAAGGAGGCGGCCAGCGGCACGTCCCAC  
LeuTyrSerGluMetGlnLeuGluAspGlyGlyArgArgArgProSerGlyThrSerHis

2710

2730

2750

AATGCCCTCAAGATTTTAGGGAACCCAGCCTCTGCAGGACGGGTGGATCACATGGGCCCG  
AsnAlaLeuLysIleLeuGlyAsnProAlaSerAlaGlyArgValAspHisMetGlyArg

2770

2790

2810

AGGTTTCCCCGTGGCAGCGCTGGTCCTCAGAGGTCCCGGCCCGTGACAGTCCCATCCATC  
ArgPheProArgGlySerAlaGlyProGlnArgSerArgProValThrValProSerIle

2830

2850

2870

GACGATTACGGGCGAGACCGCCTTTCTCCAGACTTCTATGAAGAGTCAGAACTGACCCT  
AspAspTyrGlyArgAspArgLeuSerProAspPheTyrGluGluSerGluThrAspPro

FIG. 27 E

2890	2910	2930
GGTGCCGAAGAGCTCCCGGCCCGGATCTTTGTGGCTCTCTTTGACTACGACCCGCTCACC GlyAlaGluGluLeuProAlaArgIlePheValAlaLeuPheAspTyrAspProLeuThr		
2950	2970	2990
ATGTCCCCAAACCCAGATGCTGCAGAGGAGGAGCTTCCCTTTAAAGAAGGCCAGATCATC MetSerProAsnProAspAlaAlaGluGluGluLeuProPheLysGluGlyGlnIleIle		
3010	3030	3050
AAGGTTTATGGTGATAAAGACGCTGATGGATTCTACCGTGGGGAAACCTGTGCCCGGCTT LysValTyrGlyAspLysAspAlaAspGlyPheTyrArgGlyGluThrCysAlaArgLeu		
3070	3090	3110
GGCCTTATTCCTTGTAACATGGTCTCTGAGATACAAGCAGATGATGAGGAGATGATGGAT GlyLeuIleProCysAsnMetValSerGluIleGlnAlaAspAspGluGluMetMetAsp		
3130	3150	3170
CAGCTTCTTAGACAGGGCTTTCTCCCTCTGAATACACCTGTGGAGAAAATAGAGAGAAGC GlnLeuLeuArgGlnGlyPheLeuProLeuAsnThrProValGluLysIleGluArgSer		
3190	3210	3230
AGGAGAAGTGGCAGGCGTCATTCGGTATCGACGCGGAGAATGGTGGCCCTGTATGACTAC ArgArgSerGlyArgArgHisSerValSerThrArgArgMetValAlaLeuTyrAspTyr		
3250	3270	3290
GACCCAGAGAAAGCTCGCCCAACGTCGATGTCGAGGCCGAACCTTACATTTTGCACAGGA AspProArgGluSerSerProAsnValAspValGluAlaGluLeuThrPheCysThrGly		
3310	3330	3350
GATATTATTACAGTTTTTGGTGAAATTGATGAAGATGGATTTTATTATGGGGAGCTGAAC AspIleIleThrValPheGlyGluIleAspGluAspGlyPheTyrTyrGlyGluLeuAsn		
3370	3390	3410
GGGCAGAAAGGCCTTGTGCCCTCAAACCTTCTTGAAGAAGTGCCTGATGACGTAGAAGTC GlyGlnLysGlyLeuValProSerAsnPheLeuGluGluValProAspAspValGluVal		
3430	3450	3470
TATCTTTCTGATGCTCCATCCCACTACTCTCAAGATACGCCAATGCGCTCAAAGGCAAAA		

FIG. 27 F

TyrLeuSerAspAlaProSerHisTyrSerGlnAspThrProMetArgSerLysAlaLys

3490 3510 3530  
AGGAAGAAGAGTGTTTCATTTTCATACCTTAATCAGGCAATGTAGCCTTCACGTAAGTGAGC  
ArgLysLysSerValHisPheIleProEnd

3550 3570 3590  
AACTGAAGATACCGATAAAGATACCAACTTAAGCTACCTTAACCGGGCCAGTGTGGTAGA

3610 3630 3650  
CTTAAGGCTTCATTGTGGGGTTAAAAAAGATACAAAGAAATATGTCTCAAAA

3670 3690 3710  
ACTATTGGACCTAAATAATTAGAATATTACTTGGTCTCAGTTGTAAAGCAACTGAATTTA

3730 3750 3770  
TAGTGAAGCAAATCATCTTTAATAATCATTTCTACTATTTGCATTAAGAATATTTGAAA

3790 3810 3830  
GGCCAACATTGGGAACATATTTCTTAACAAGCTAACTGTGTGTTTACATAGAGAGAGCTG

3850 3870 3890  
CATATTGCATTGTTAGCCACTCTTGGAAGAGCACAACCTAACAAACATGTTTACTATAG

3910 3930 3950  
GAAGCTTTACTTTAGAACTTAACCCAAGGTCAAGCAGATGAGTAGTGAACACAGGTGAT

3970 3990 4010  
CGAGTGTTGGCTCTGAACACTCCAAACACTGGCTCGAGTGGCCAGAACGTGTTTTCCTTA

4030 4050 4070  
AGTAACCCTGCCTCTACCTTACGAGAGAGCTATGCTCCTCCTCAAAGCACAATCATCCTG

4090 4110 4130  
TGACAGAAGTTGCTGCAACACGCGTTTGTGTGGTATACCAATGCAATACTAAGTTGAT

FIG. 27 G



4150	4170	4190
GAAGCACGCAGCTCAAATGATCACATTAGATGGAATAGATGGTATCTTCAGGTGTACTTT		
4210	4230	4250
GGGATGCTTTACTAGGTGTTTTCCATTAGAATTAGACCTTGATTTTAAATCCAAGCAAGC		
4270	4290	4310
TTGAAGCCCCTTGGCTTACAGCATTGCTGCTGAATACTAAACACTCACATGGCAAGAG		
4330	4350	4370
TTGCTCTGGAGAGGTAGGGCCAGAGGAATGCTGCTGCACTGCCAACTCAGGCACATGCTT		
4390	4410	4430
AGCTGTAAAGGGAAGCGAGGTGAAGTCGTCCTGCAGCGTATTAGAGTAAAAGTCTACCCC		
4450	4470	4490
TCTGAAGCACTATTAAGCGCTTAACGTATATTTAAATACTACCATGTGCTATCTACTGAG		
4510	4530	4550
GAAGATTCATGTTCAATTATTTGGAAATAATGCAAGCATCCACTAAGGGCCTTTAAGCTT		
4570	4590	4610
TCTTTGATTATAATTAAGGTTCATTTTAGTTTTTTTTTTTTCTTTCAACCAGTGTGCCAT		
4630	4650	4670
CTCCAATATTTCTATAGTATACCAACCACCCCAGGAATGCACTTTAACAATATCAGGATT		
4690	4710	4730
TTATATAACCAAATAGTTTCAAATACAACAAAATTCCTTTATGAACTTTCGCTTTTAA		
4750	4770	4790
GACTACTGATGGGTACTCGGCCAACTTTACTATCAACCTAATTCAGATCATGTCTCCCC		

FIG. 27 H

4810	4830	4850
TGCCCTTAGTCTTCATTTATGAAGTGAATTATTACCTGCCTTAGCTTTGCCAAAGCAACG		
4870	4890	4910
GCCACCCCGCACTCCCTCGAGACAGAGAAACGGAACCCACACATTTATGTCTGGGGCCTC		
4930	4950	4970
TCTCTGGCGTGCTGTGGGAGAGGACCTTTGCTTCTCATGGCATACTTCAACAACCTGAAAG		
4990	5010	5030
AACAAATGAACCCCCCTGACCTTTCCTGGTGGGAAACGGGGACAGTACGATGTTACCAAG		
5050	5070	5090
TGAATTCTGTTGTTGGCGCTCACACACTCAATAAACTGTAACTGTACCTACTAGGTTTC		
5110	5130	5150
CTCCTGAGGGTTCAGGTACAGCAAGGAGAGCTCCATCCCCACAGTCCATCTCCATTTCGG		
5170	5190	5210
GGTCACCTACGTCATCTATGGGTTCTGGTAGTCCTGGGAGAGGCAGGGAAATGTCCTCGA		
5230	5250	5270
AAAAGAAAAAGGGGCTGCTTTCCAAAGGCAAGAACTGCTGAAAAGCTGGGTGCAGTGA		
5290	5310	5330
AATGATTCATGTGCTTCCGGACAACCTGCCAAATCTATGTAATTTCTTTAATTCCAAACT		
5350	5370	5390
AGGGCTTTCATGACTCAAGTACTTCCTAAAAAACCCAATCTTCTCCCCTGACACCAGTA		
5410	5430	5450
GAGAAATGCACCTTTTGCACCTACCAACCACTTTAAACCAACCACGAGAACAAAGAGGAGCG		
5470	5490	5510

FIG. 27 I

GTTGCTCTCTGTCACCGCTGGCAGTCTGCTCTCATTGTCCAAGCTCTGATTGGGAGGTG

5530

5550

5570

GGAGGGGACGTCTTATTAACAAACGGGGGCGCATAGCTATCACCTGTAGCTCCCTCCCTA

5590

5610

5630

CCTGTAATTCCAGTCTTTGTGCATTTGTCATCTGCCCTTAAAGGAATGATTTTCAACCTT

5650

5670

5690

TCTCCCTTCTCAAATGCTTGCCTCATAATGCATAACTTCACTTTGACTCTGGTCTTGA

5710

5730

5750

AATTCCTAGTTTAATTGCGCTTGATGTTCTGCCTTATAAATGCACAATGATTTGTACTGT

5770

5790

5810

CTAATAAAAACAGTGTATACTTTGTATGTGTCGTGCATTCACTGGTCTTCATCCTGACAC

5830

5850

5870

AGTGGTTCGAGATCAAGTTGTACAGGCTGTGCATTTTAAGATACTAGTTTCAGTCTTTCA

5890

5910

5930

AAGCCAGCCAGGCTACACACAGAAAATGTTTACTCAATCATTCAAAAAGAGAAAAGGAG

5950

5970

5990

AGAAAGTAACTTTGTTTGGTAAAGCACCAGTACTCCAACCTTCCAGAAAGCCGATTATCT

6010

6030

6050

TCATTGCTTTTAATGTTCTATTCTGTGGCATATGGTTTTCTGTTACTTTCTGTTGTCAAAA

6070

6090

6110

TGCCATACCCAAATACACAGCAATGAATGGCACACAAGTAATCCACATAATGCATAAGCC

6130

6150

6170

ACACCAAACCAGACTCAATTTAAATCTGCTCCAAATGAGTCCATACCCATCTTCATCAT

FIG. 27 J

6190	6210	6230
TGGCATTGAAACAAAAGACTTACTTACAAAGTTGCTGGCAGATGTATTTGATGGTTACTC		
6250	6270	6290
TTTTGTAATTCTTGTCCACTTGTAATTGTTTTACTCTTTATACATACTTTTCAGACTG		
6310	6330	6350
CCTTTCTTTTGTAATTTATGGACGGTTTATAAATGAATGACAAAGCTTTCCCCATTGTGT		
6370	6390	6410
CTTCAAAAACGCTATTATAAATTGTAATATAATAGTATGTGGTAGATTTATTATTAAAGG		
6430	6450	6470
AAATCCATGTGTGGTTAAGCTCTGTGTGGGTGTGTGCATGTGCACAGTTAGTGTAATAA		
6490		
TTTTCTAGAAATAAAATTTGTTATTTTAT		

FIG. 27 K

10	30	50
GGTCCCCACGCCAGGATGGATGAGGCCTGGGAGCAGAAGCCTGTGCACCTGGCCCTGTGC		
MetAspGluAlaTrpGluGlnLysProValHisLeuAlaLeuCys		
70	90	110
ATGGGCACATGCTGGAGCCGCCCGTGGGCCCCGCATCCTGCCACAGCCACAGGGCACCCC		
MetGlyThrCysTrpSerArgProTrpAlaProHisProAlaThrAlaThrGlyHisPro		
130	150	170
GGTGTCCACCACCGTCGCCAAGGCCATGGCCCCGGGAGGCCGCGCAGAGGGTGGCGAGAGC		
GlyValHisHisArgArgGlnGlyHisGlyProGlyGlyArgAlaGluGlyGlyGluSer		
190	210	230
AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGCGGGGCAGTACGCCGCC		
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla		
250	270	290
TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC		
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp		
310	330	350
GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGGGAAACTGAGGCCACAGAATTGAGAA		
AspPheLeuLysGlySerGluLeuGlyLysGlnGlyAsnEnd		
370	390	410
TTTTTGTCATGATTACGCAGATGGTCTCCTAACAGAGCTGGAATTAGATTGAACCGAGG		
430	450	470
CCTGAAGAAGACCTGTTTCCACGCCTTTCCCATGTGCCACGTTCTCCTCACCTATCCAG		
490	510	530
GAGTGAATCATCACCTTCCCTGCAATCTGCTCAGGTTACAAACCCGGAGGAAAGGCTGGA		
550	570	590
GCACTTGTTCTCTGGGTGAAGGACCCATACCCCCACTGGTTTTTGAGATCGGCATTTCAGC		

FIG. 28 A

610	630	650
GCTGTCTTATGGCAGCCMCAGCCCCAGGTGGCCCCAGAGCCCTTGACATGTGGCCACCTG		
670	690	710
GGGCTGAGTGTGACTGAGGCCCTGAATTTTACTTCTATAAAATTAGTTCAGATTAGTT		
730	750	770
TACATTCCTAATTAGTTTACATGTAAACAGCCACACGTGGCTGGTGGCCACCAGTGCTGA		
790	810	830
CGCCCAGCTCTGGATGACCACACCTGCTACAAGAGATGACTTTTCTAGAGAAGAGTAGAA		
850	870	890
ACACAGCGGCAGAAACACAGCTCTGCACTTCCGAGGGCCTCCCACTCCTTCTGATGAGAC		
910	930	950
TGCAGAGGAAGTCTGTTTGGCCAAGCATGCTATTAACACGTTTTCCTGCTTGTTTTGTTT		
970	990	1010
TTTAACAGAGCAAACAGGTCTGTTTCTATTAAAATTTAAAAGCGTTAATATTTARCAGC		
1030	1050	1070
ATTGTTTTATGTTGTATTCATAACATAATAATATAACAATATATTAATTGTTAATATATA		
1090	1110	1130
TTGTTAATAATATAATAATATAACATAAAATAAGTGATACTTATTTTCCATTACAGTTG		
1150	1170	1190
AGATATTTTCTTTAAAAGTAACGTAAATATTGATTCAATTCAAAGAATACATTCATTAA		
1210	1230	1250
TCATACAGATGGCGTCTGGCTAGGTGACGCATCATGACAGTGGTAGGGAGTGACTGAAGT		
1270	1290	1310

FIG. 28 B

TGAGCTGGTGCACAGACTGCCAGTTTTACAAACCCGGGAAGTGTTCCCTGACCATCCGCTT  
 1330 1350 1370  
 CCCCATGCTGCCCCGCCCCGTCACATGAGCCCTTACCCCCTGGCGCTATCCCATCTGCTCC  
 1390 1410 1430  
 AAGACACCGATGTTCTAGTGGGTGGAAGCCTCCACTTTTAGTTGACTACGGTATCTCTAG  
 1450 1470 1490  
 CATTTCACACATAGTAGGTGCTCAATGAATGTTTGTCGAATGAATGAATGAAAGAAGGGA  
 1510 1530 1550  
 GGCTGAGAGTAGCTGGGACATTTGCTCTGAAAAAATCACCTCCATTCTCCCAATATTACA  
 1570 1590 1610  
 AAAGCATTTTCATTAAGTCCACAATGAAAAATGCTCACTGTACCAATAAATAATATCTTT  
 1630 1650  
 AGTTATCTATTTTTTAAAAGTAAAAAAAACCTCGTGCCGAAGTC

FIG. 28 C